

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:18 ; Search time 29.648 Seconds
(without alignments)
165.965 Million cell updates/sec

Title: US-09-843-221A-165
Perfect score: 31
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size : 0

Total number of hits satisfying chosen parameters: 75810

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : A_Geneseq_19Jun03:*

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- 23: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2002.DAT:*
- 24: /SIDS1/gcgdata/geneseq/geneseqp-embl/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	% Query Match	Length	DB	ID	Description
	1	31	100.0	31	19	AAW42059	Human parathyroid
	2	31	100.0	31	19	AAW42051	Human parathyroid
	3	31	100.0	31	20	AAAY02578	N-terminal 31 resi
	4	31	100.0	31	22	AAB81080	Human parathyroid
	5	31	100.0	31	22	AAB91097	Parathyroid hormon
	6	31	100.0	31	23	AAE23720	Human parathyroid
	7	31	100.0	31	23	AAU73039	Parathyroid hormon
	8	31	100.0	32	23	AAU73176	Parathyroid hormon
	9	31	100.0	33	21	AAAY98018	Human amino-termin
	10	31	100.0	34	4	AAP30022	Human parathyroid-
	11	31	100.0	34	6	AAP50377	[Met(O)8,18]hPTH-(
	12	31	100.0	34	7	AAP60031	Sequence of the fi
	13	31	100.0	34	11	AAR07919	Human parathyroid
	14	31	100.0	34	11	AAR07922	Human parathyroid
	15	31	100.0	34	13	AAR22283	Parathyroid hormon
	16	31	100.0	34	14	AAR41549	[D-Ser3]hPTH (1-34
	17	31	100.0	34	14	AAR41570	[Gln25]hPTH (1-34)
	18	31	100.0	34	15	AAR58291	[Lys(For)26, Lys(F
	19	31	100.0	34	15	AAR58228	[D-Asp30]-hPTH(1-3
	20	31	100.0	34	15	AAR58232	[Lys32]-hPTH(1-34)
	21	31	100.0	34	15	AAR58181	[Thr33, Ala34]-hPT
	22	31	100.0	34	15	AAR58016	N-alpha-Isopropyl-
	23	31	100.0	34	15	AAR58017	[Lys(N-epsilon-Iso
	24	31	100.0	34	15	AAR55724	Parathormone N-ter
	25	31	100.0	34	16	AAR74521	Human parathyroid
	26	31	100.0	34	17	AAW99449	Human parathyroid
	27	31	100.0	34	17	AAR99978	Human parathyroid
	28	31	100.0	34	17	AAR98951	Target peptide (PT
	29	31	100.0	34	17	AAR98966	PTH(1-34). Not sp
	30	31	100.0	34	17	AAR88835	Human parathyroid
	31	31	100.0	34	18	AAW24273	Wild type parathyr
	32	31	100.0	34	18	AAW19994	Cyclised human par
	33	31	100.0	34	18	AAW20000	Cyclised human par
	34	31	100.0	34	18	AAW20006	Cyclised human par
	35	31	100.0	34	18	AAW17955	Human parathyroid
	36	31	100.0	34	19	AAW67291	Parathyroid hormon
	37	31	100.0	34	19	AAW61658	Parathyroid hormon
	38	31	100.0	34	19	AAW65975	Human parathyroid
	39	31	100.0	34	19	AAW42614	Human parathyroid
	40	31	100.0	34	19	AAW48392	Human parathyroid
	41	31	100.0	34	20	AAAY50593	Resin bound cyclic
	42	31	100.0	34	20	AAAY17752	Human parathyroid
	43	31	100.0	34	20	AAAY14151	Human parathyroid
	44	31	100.0	34	20	AAAY02579	N-terminal 34 resi
	45	31	100.0	34	20	AAW81871	Human PTH N-termin
	46	31	100.0	34	21	ABJ10712	Human parathyroid
	47	31	100.0	34	21	AAB07454	Amino acids 1-34 o
	48	31	100.0	34	21	AAAY98017	Human amino-termin
	49	31	100.0	34	21	AAAY82631	Human parathyroid
	50	31	100.0	34	21	AAAY68763	Amino acids 1-34 o

51	31	100.0	34	22	AAB84778	Native rat parathy
52	31	100.0	34	22	AAB96898	Human parathyroid
53	31	100.0	34	22	AAB96929	Human parathyroid
54	31	100.0	34	22	AAB81079	Human parathyroid
55	31	100.0	34	22	AAB91098	Parathyroid hormon
56	31	100.0	34	23	ABJ05328	Human PTH(1-34) pe
57	31	100.0	34	23	AAE23727	Human parathyroid
58	31	100.0	34	23	ABB06329	Human parathyroid
59	31	100.0	34	23	ABB08595	C-terminal truncat
60	31	100.0	34	23	AAE18395	Human PTH peptide
61	31	100.0	34	23	ABB07147	Parathyroid hormon
62	31	100.0	34	23	AAU73028	Parathyroid hormon
63	31	100.0	34	24	ABP71500	Human parathyroid
64	31	100.0	34	24	ABG74235	Human parathyroid
65	31	100.0	35	22	AAB91112	Parathyroid hormon
66	31	100.0	35	23	AAU73172	Parathyroid hormon
67	31	100.0	36	14	AAR39450	Ser-Val- (hPTH 3-35
68	31	100.0	36	15	AAR58286	[D-Leu24] -hPTH(1-3
69	31	100.0	36	15	AAR58292	[D-Lys27] -hPTH(1-3
70	31	100.0	36	15	AAR58293	[D-Leu28] -hPTH(1-3
71	31	100.0	36	15	AAR58294	[D-Phe34] -hPTH(1-3
72	31	100.0	36	15	AAR58295	[D-Val35] -hPTH(1-3
73	31	100.0	36	15	AAR58296	[Ala35] -hPTH(1-36)
74	31	100.0	36	15	AAR58297	[Pro35] -hPTH(1-36)
75	31	100.0	36	15	AAR58298	[NMeVal35] -hPTH(1-
76	31	100.0	36	15	AAR58299	[Thr35,Ala36] -hPTH
77	31	100.0	36	15	AAR58300	[D-Ala36] -hPTH(1-3
78	31	100.0	36	15	AAR58301	[NMeAla36] -hPTH(1-
79	31	100.0	36	15	AAR58260	[D-Val2] -hPTH(1-36
80	31	100.0	36	15	AAR58263	[D-Ile5] -hPTH(1-36
81	31	100.0	36	15	AAR58264	[D-Gln6] -hPTH(1-36
82	31	100.0	36	15	AAR58265	[D-Leu7] -hPTH(1-36
83	31	100.0	36	15	AAR58270	[D-Leu11] -hPTH(1-3
84	31	100.0	36	15	AAR58272	[D-Lys13] -hPTH(1-3
85	31	100.0	36	15	AAR58273	[D-Leu15] -hPTH(1-3
86	31	100.0	36	15	AAR58276	[Met (O2) 18] -hPTH(1
87	31	100.0	36	15	AAR58278	[D-Met18] -hPTH(1-3
88	31	100.0	36	15	AAR58280	[D-Arg20] -hPTH(1-3
89	31	100.0	36	15	AAR58281	[D-Val21] -hPTH(1-3
90	31	100.0	36	15	AAR58284	[D-Trp23] -hPTH(1-3
91	31	100.0	36	15	AAR58227	[D-Gln29] -hPTH(1-3
92	31	100.0	36	15	AAR58230	[D-Val31] -hPTH(1-3
93	31	100.0	36	15	AAR58233	[D-His32] -hPTH(1-3
94	31	100.0	36	15	AAR58234	[Ala32] -hPTH(1-36)
95	31	100.0	36	15	AAR58235	[D-Asn33] -hPTH(1-3
96	31	100.0	36	15	AAR58236	[Ala33] -hPTH(1-36)
97	31	100.0	36	15	AAR58237	[NMePhe34] -hPTH(1-
98	31	100.0	36	15	AAR58238	[D-Asp30] -hPTH(1-3
99	31	100.0	36	15	AAR58242	[Lys (Isopropyl) 13]
100	31	100.0	36	15	AAR58246	Acetyl-hPTH(1-36) -
101	31	100.0	36	15	AAR58249	[D-Ser1] -hPTH(1-36
102	31	100.0	36	15	AAR58191	[Ala34] -hPTH(1-36)
103	31	100.0	36	15	AAR58196	[D-Phe34, D-Ala36]
104	31	100.0	36	15	AAR58198	[D-Ser3] -hPTH(1-36
105	31	100.0	36	15	AAR58199	[D-Glu4] -hPTH(1-36
106	31	100.0	36	15	AAR58200	[D-His9] -hPTH(1-36
107	31	100.0	36	15	AAR58202	[D-Asn10] -hPTH(1-3

108	31	100.0	36	15	AAR58210	[D-His14]-hPTH(1-3
109	31	100.0	36	15	AAR58211	[D-Asn16]-hPTH(1-3
110	31	100.0	36	15	AAR58213	[D-Ser17]-hPTH(1-3
111	31	100.0	36	15	AAR58215	[D-Glu19]-hPTH(1-3
112	31	100.0	36	15	AAR58220	[D-Lys26]-hPTH(1-3
113	31	100.0	36	15	AAR58171	[N-Me-Ser1]-hPTH(1
114	31	100.0	37	12	AAR11882	Parathyroid hormon
115	31	100.0	37	13	AAR24778	hPTH(1-37)-amide/e
116	31	100.0	37	15	AAR58244	[Ala0]-hPTH(1-36)-
117	31	100.0	37	15	AAR58245	[Pro0]-hPTH(1-36)-
118	31	100.0	37	22	AAB86226	Human parathyroid
119	31	100.0	37	22	AAB86229	Human parathyroid
120	31	100.0	37	23	ABB82203	Human parathyroid
121	31	100.0	38	3	AAP20248	Parathyroid hormon
122	31	100.0	38	15	AAR58282	[Trp(SO2Pmc)23]-hP
123	31	100.0	38	15	AAR58283	[Trp(Pmc)23]-hPTH(
124	31	100.0	38	15	AAR58018	Isopropyl-[Lys(Iso
125	31	100.0	38	15	AAR58162	[Arg33]-hPTH(1-38)
126	31	100.0	38	15	AAR58163	[Pro33]-hPTH(1-38)
127	31	100.0	38	15	AAR58164	[Asp33]-hPTH(1-38)
128	31	100.0	38	15	AAR58165	[Ile33]-hPTH(1-38)
129	31	100.0	38	15	AAR58166	[Lys33]-hPTH(1-38)
130	31	100.0	38	15	AAR58075	[Ser33]-hPTH(1-38)
131	31	100.0	38	15	AAR58076	[Thr33]-hPTH(1-38)
132	31	100.0	38	15	AAR58077	[Leu33]-hPTH(1-38)
133	31	100.0	38	15	AAR58078	[Gly33]-hPTH(1-38)
134	31	100.0	38	15	AAR58084	[Gln33]-hPTH(1-38)
135	31	100.0	38	15	AAR54234	PTH N-terminal. S
136	31	100.0	38	20	AAV02580	N-terminal 38 resi
137	31	100.0	38	22	AAB91101	Parathyroid hormon
138	31	100.0	38	23	AAE23729	Human parathyroid
139	31	100.0	38	23	AAE18400	Human PTH peptide
140	31	100.0	38	23	AAU73026	Parathyroid hormon
141	30	96.8	30	17	AAR88832	Human parathyroid
142	30	96.8	30	23	AAU73051	Parathyroid hormon
143	30	96.8	31	23	AAU73177	Parathyroid hormon
144	30	96.8	33	21	AAV98012	Human amino-termin
145	30	96.8	33	21	AAV98015	Human amino-termin
146	30	96.8	34	18	AAW17948	Human parathyroid
147	30	96.8	34	18	AAW17968	Human parathyroid
148	30	96.8	34	19	AAW67283	Parathyroid hormon
149	30	96.8	34	21	AAV98010	Human amino-termin
150	30	96.8	34	21	AAV98011	Human amino-termin
151	30	96.8	34	21	AAV98014	Human amino-termin
152	30	96.8	34	22	AAB91113	Parathyroid hormon
153	30	96.8	34	23	AAE23728	Human parathyroid
154	30	96.8	34	23	AAE18399	Human PTH peptide
155	30	96.8	34	23	AAU73032	Parathyroid hormon
156	30	96.8	36	12	AAR15842	Human parathyroid
157	30	96.8	36	13	AAR23995	Human paprthyroid
158	30	96.8	36	15	AAR58254	[4-aminosalicylic
159	30	96.8	36	15	AAR58255	[TMSA1]-hPTH(1-36)
160	30	96.8	36	15	AAR58256	[Phe1]-hPTH(1-36)-
161	30	96.8	36	15	AAR58257	[Propargylglycin1]
162	30	96.8	36	15	AAR58262	[Ala1]-hPTH(1-36)-
163	30	96.8	36	15	AAR58231	[Ala31]-hPTH(1-36)
164	30	96.8	36	15	AAR58243	Propargyl-[A1]-hPT

165	30	96.8	36	15	AAR58247	[Hyp1]-hPTH(1-36)-
166	30	96.8	36	15	AAR58248	N-Dimethyl-[Ala1]-
167	30	96.8	36	15	AAR58250	[Lys(For)1]-hPTH(1
168	30	96.8	36	15	AAR58251	[D-glyceric acid1]
169	30	96.8	36	15	AAR58252	[Asn1]-hPTH(1-36)-
170	30	96.8	36	15	AAR58253	[4-aminobenzoic ac
171	30	96.8	36	15	AAR58169	[D-Pro1]-hPTH(1-36
172	30	96.8	36	15	AAR58170	[Nva1]-hPTH(1-36)-
173	30	96.8	36	15	AAR58172	[Indole-2-carboxyl
174	30	96.8	36	15	AAR58173	[Indole-3-carboxyl
175	30	96.8	36	15	AAR58174	[Pyridine-3-carbox
176	30	96.8	36	15	AAR58175	[Pyridine-2-carbox
177	30	96.8	36	15	AAR58176	[Hexahydropyridazi
178	30	96.8	36	15	AAR58177	[Morpholine-2-carb
179	30	96.8	36	15	AAR58178	[Pro1]-hPTH(1-36)-
180	30	96.8	36	15	AAR58179	[Leu1]-hPTH(1-36)-
181	30	96.8	36	15	AAR58180	[Ile1]-hPTH(1-36)-
182	30	96.8	36	15	AAR58026	N-alpha-methyl [Ala
183	30	96.8	36	15	AAR58168	[1-amino-cyclopent
184	30	96.8	37	23	AAU73027	Parathyroid hormon
185	30	96.8	38	15	AAR58019	N-alpha-methyl [Ala
186	30	96.8	38	15	AAR58022	[Ile1]-hPTH(1-38)-
187	30	96.8	38	15	AAR58028	[Thr1]-hPTH(1-38)-
188	30	96.8	38	15	AAR58029	[Leu1]-hPTH(1-38)-
189	30	96.8	38	15	AAR58030	[Abu1 or Gabal]-hP
190	30	96.8	38	15	AAR58167	[Ile31,Arg33]-hPTH
191	29	93.5	29	17	AAR88836	Human parathyroid
192	29	93.5	29	23	AAU73063	Parathyroid hormon
193	29	93.5	30	23	AAU73055	Parathyroid hormon
194	29	93.5	30	23	AAU73178	Parathyroid hormon
195	29	93.5	32	5	AAP40427	Parathyroid antago
196	29	93.5	34	22	AAB61638	Peptide #1 that ca
197	29	93.5	36	15	AAR58259	[aBU2]-hPTH(1-36)-
198	29	93.5	36	15	AAR58261	[Tert.Leu]-hPTH(1-
199	29	93.5	36	15	AAR58229	[Ala30]-hPTH(1-36)
200	29	93.5	38	15	AAR58023	[Ala1,Abu2 or Nva2
201	29	93.5	38	15	AAR58024	[Ala1,Ile2]-hPTH(1
202	28	90.3	28	17	AAR88837	Human parathyroid
203	28	90.3	28	21	AAV98052	Human parathyroid
204	28	90.3	28	23	AAU73064	Parathyroid hormon
205	28	90.3	29	12	AAR11731	Adenine-rich PTH-(
206	28	90.3	29	23	AAU73179	Parathyroid hormon
207	28	90.3	31	5	AAP40760	Human parathyroid
208	28	90.3	34	14	AAR41550	[D-Ala3]hPTH (1-34
209	28	90.3	34	18	AAW17957	Human parathyroid
210	28	90.3	34	18	AAW01610	Parathryoid hormon
211	28	90.3	34	19	AAW67293	Parathyroid hormon
212	28	90.3	36	15	AAR58190	[Ala29]-hPTH(1-36)
213	28	90.3	36	15	AAR58197	[Ala3]-hPTH(1-36)-
214	28	90.3	38	15	AAR58161	[Pro3,Thr33]-hPTH(
215	27	87.1	28	21	AAV98048	Human parathyroid
216	27	87.1	28	21	AAV98050	Human parathyroid
217	27	87.1	30	23	AAE23752	Human parathyroid
218	27	87.1	32	23	AAE23735	Human parathyroid
219	27	87.1	34	18	AAW17947	Human parathyroid
220	27	87.1	34	18	AAW17951	Human parathyroid
221	27	87.1	34	19	AAW67282	Parathyroid hormon

222	27	87.1	34	19	AAW67286	Parathyroid hormon
223	27	87.1	38	15	AAR58159	[Val28]-hPTH(1-38)
224	27	87.1	38	15	AAR58160	[Ile28]-hPTH(1-38)
225	26	83.9	28	17	AAR88838	Human parathyroid
226	26	83.9	28	22	AAB81074	Human parathyroid
227	26	83.9	29	17	AAR88839	Human parathyroid
228	26	83.9	29	22	AAB81075	Human parathyroid
229	26	83.9	30	17	AAR88833	Human parathyroid
230	26	83.9	30	19	AAW42052	Human parathyroid
231	26	83.9	30	23	AAU73062	Parathyroid hormon
232	26	83.9	31	19	AAW42056	Human parathyroid
233	26	83.9	31	19	AAW42057	Human parathyroid
234	26	83.9	31	19	AAW42060	Human parathyroid
235	26	83.9	31	19	AAW42062	Human parathyroid
236	26	83.9	31	19	AAW42067	Human parathyroid
237	26	83.9	31	19	AAW42049	Human parathyroid
238	26	83.9	31	19	AAW42050	Human parathyroid
239	26	83.9	31	19	AAW42053	Human parathyroid
240	26	83.9	31	23	AAU73040	Parathyroid hormon
241	26	83.9	31	23	AAU82640	Analogue of human
242	26	83.9	34	13	AAR22298	Human parathyroid
243	26	83.9	34	13	AAR22299	Human parathyroid
244	26	83.9	34	14	AAR41554	[Thr27]hPTH (1-34)
245	26	83.9	34	14	AAR41555	[Asn27]hPTH (1-34)
246	26	83.9	34	14	AAR41558	[Ser27]hPTH (1-34)
247	26	83.9	34	14	AAR41559	[Gly27]hPTH (1-34)
248	26	83.9	34	14	AAR41560	[His27]hPTH (1-34)
249	26	83.9	34	17	AAR88829	Human parathyroid
250	26	83.9	34	17	AAR88834	Human parathyroid
251	26	83.9	34	18	AAW17969	Human parathyroid
252	26	83.9	34	19	AAW67290	Parathyroid hormon
253	26	83.9	34	19	AAW67292	Parathyroid hormon
254	26	83.9	34	19	AAW67297	Parathyroid hormon
255	26	83.9	34	19	AAW42054	Human parathyroid
256	26	83.9	34	19	AAW42055	Human parathyroid
257	26	83.9	36	15	AAR58222	[His27]-hPTH(1-36)
258	26	83.9	36	15	AAR58223	[Phe27]-hPTH(1-36)
259	26	83.9	36	15	AAR58224	[Nle27]-hPTH(1-36)
260	26	83.9	36	15	AAR58225	[Asn27]-hPTH(1-36)
261	26	83.9	36	15	AAR58226	[Ala27]-hPTH(1-36)
262	26	83.9	38	15	AAR58154	[Val27]-hPTH(1-38)
263	26	83.9	38	15	AAR58155	[Ile27]-hPTH(1-38)
264	26	83.9	38	15	AAR58156	[Leu27]-hPTH(1-38)
265	26	83.9	38	15	AAR58157	[Arg27]-hPTH(1-38)
266	26	83.9	38	15	AAR58158	[Ala27]-hPTH(1-38)
267	25	80.6	28	13	AAR22064	Modified hPTH(7-34
268	25	80.6	28	13	AAR22065	Modified [Tyr ₃₄]h
269	25	80.6	28	23	AAE23734	Human parathyroid
270	25	80.6	28	23	AAU73044	Parathyroid hormon
271	25	80.6	32	21	AAB07468	Antigenic peptide
272	25	80.6	34	14	AAR41556	[Gln26,27]hPTH (1-
273	25	80.6	34	14	AAR41566	[Arg 26,27]hPTH (1
274	25	80.6	34	14	AAR41567	[Gln26]hPTH (1-34)
275	25	80.6	34	18	AAW01609	Parathryoid hormon
276	25	80.6	36	15	AAR58290	[Ala26]-hPTH(1-36)
277	25	80.6	36	15	AAR58218	[Gln26]-hPTH(1-36)
278	25	80.6	36	15	AAR58219	[Nle26]-hPTH(1-36)

279	25	80.6	38	15	AAR58153	[Arg26]-hPTH(1-38)
280	25	80.6	38	17	AAR98958	Target peptide (PT
281	24	77.4	31	17	AAR88830	Human parathyroid
282	24	77.4	32	17	AAR88840	Human parathyroid
283	24	77.4	33	17	AAR88841	Human parathyroid
284	24	77.4	34	14	AAR34456	Human parathyroid
285	24	77.4	34	14	AAR34457	Human parathyroid
286	24	77.4	34	14	AAR41557	[Gln25,26,27]hPTH
287	24	77.4	34	18	AAW17943	Human parathyroid
288	24	77.4	34	19	AAW67278	Parathyroid hormone
289	24	77.4	36	15	AAR58287	[Phe25]-hPTH(1-36)
290	24	77.4	36	15	AAR58288	[Lys25]-hPTH(1-36)
291	24	77.4	36	15	AAR58289	[Ala25]-hPTH(1-36)
292	24	77.4	36	15	AAR58192	[Gln25]-hPTH(1-36)
293	23	74.2	28	21	ABJ10776	Human parathyroid
294	23	74.2	34	13	AAR22293	Human parathyroid
295	23	74.2	34	15	AAR49697	Sequence of varian
296	23	74.2	34	15	AAR49698	Sequence of varian
297	23	74.2	34	18	AAW17949	Human parathyroid
298	23	74.2	34	18	AAW17945	Human parathyroid
299	23	74.2	34	18	AAW17950	Human PTH analogue
300	23	74.2	34	19	AAW67280	Parathyroid hormone
301	23	74.2	34	19	AAW67284	Parathyroid hormone
302	23	74.2	34	19	AAW67285	Parathyroid hormone
303	23	74.2	34	19	AAW67288	Parathyroid hormone
304	23	74.2	34	19	AAW67289	Parathyroid hormone
305	23	74.2	34	19	AAW67294	Parathyroid hormone
306	23	74.2	34	19	AAW67295	Parathyroid hormone
307	23	74.2	34	19	AAW67296	Parathyroid hormone
308	23	74.2	34	19	AAW67299	Parathyroid hormone
309	23	74.2	34	19	AAW67303	Parathyroid hormone
310	23	74.2	34	21	ABJ10706	Human parathyroid
311	23	74.2	34	21	ABJ10714	Human parathyroid
312	23	74.2	34	21	ABJ10717	Human parathyroid
313	23	74.2	34	21	ABJ10719	Human parathyroid
314	23	74.2	34	21	ABJ10722	Human parathyroid
315	23	74.2	34	21	ABJ10724	Human parathyroid
316	23	74.2	34	21	ABJ10727	Human parathyroid
317	23	74.2	34	21	ABJ10729	Human parathyroid
318	23	74.2	34	21	ABJ10730	Human parathyroid
319	23	74.2	34	21	ABJ10733	Human parathyroid
320	23	74.2	34	21	ABJ10736	Human parathyroid
321	23	74.2	34	21	ABJ10772	Human parathyroid
322	23	74.2	34	21	ABJ10773	Human parathyroid
323	23	74.2	36	15	AAR58266	[Nle8]-hPTH(1-36)-
324	23	74.2	36	15	AAR58267	[Phe8]-hPTH(1-36)-
325	23	74.2	36	15	AAR58268	[Cha8]-hPTH(1-36)-
326	23	74.2	36	15	AAR58182	[Nva8]-hPTH(1-36)-
327	23	74.2	38	15	AAR58269	[Leu8]-hPTH(1-38)-
328	22	71.0	30	23	AAU73136	Parathyroid hormone
329	22	71.0	30	23	AAU73137	Parathyroid hormone
330	22	71.0	33	9	AAP82176	Sequence of parath
331	22	71.0	34	14	AAR34358	Human parathyroid
332	22	71.0	34	14	AAR34353	Human parathyroid
333	22	71.0	34	14	AAR34354	Human parathyroid
334	22	71.0	34	14	AAR34355	Human parathyroid
335	22	71.0	34	14	AAR34356	Human parathyroid

336	22	71.0	34	14	AAR34357	Human parathyroid
337	22	71.0	34	14	AAR34359	Human parathyroid
338	22	71.0	34	14	AAR34360	Human parathyroid
339	22	71.0	34	14	AAR34361	Human parathyroid
340	22	71.0	34	14	AAR34362	Human parathyroid
341	22	71.0	34	14	AAR34363	Human parathyroid
342	22	71.0	34	14	AAR34364	Human parathyroid
343	22	71.0	34	14	AAR34365	Human parathyroid
344	22	71.0	34	14	AAR34366	Human parathyroid
345	22	71.0	34	14	AAR34367	Human parathyroid
346	22	71.0	34	14	AAR34368	Human parathyroid
347	22	71.0	34	15	AAR58187	[Phe23,His25,His26
348	22	71.0	34	15	AAR58189	[F23,H25,H26,L27,I
349	22	71.0	34	18	AAW17944	Human parathyroid
350	22	71.0	34	19	AAW67279	Parathyroid hormon
351	22	71.0	34	22	AAB91085	Parathyroid hormon
352	22	71.0	34	23	AAU73100	Parathyroid hormon
353	22	71.0	34	23	AAU73101	Parathyroid hormon
354	22	71.0	36	15	AAR58285	[Ala23]-hPTH(1-36)
355	22	71.0	36	15	AAR58188	[Phe23]-hPTH(1-36)
356	21	67.7	30	23	AAU73138	Parathyroid hormon
357	21	67.7	30	23	AAU73139	Parathyroid hormon
358	21	67.7	31	19	AAW42063	Human parathyroid
359	21	67.7	31	19	AAW42065	Human parathyroid
360	21	67.7	31	19	AAW42066	Human parathyroid
361	21	67.7	34	17	AAW15812	[Trp(10)]-hPTH(1-3
362	21	67.7	34	18	AAW08120	Human PTH derivati
363	21	67.7	34	18	AAW08109	Human parathyroid
364	21	67.7	34	18	AAW08114	Human PTH derivati
365	21	67.7	34	18	AAW08118	Human PTH derivati
366	21	67.7	34	18	AAW08119	Human PTH derivati
367	21	67.7	34	19	AAW67305	Parathyroid hormon
368	21	67.7	34	19	AAW67302	Parathyroid hormon
369	21	67.7	34	19	AAW67304	Parathyroid hormon
370	21	67.7	34	23	AAU73102	Parathyroid hormon
371	21	67.7	34	23	AAU73103	Parathyroid hormon
372	21	67.7	34	23	AAU73104	Parathyroid hormon
373	21	67.7	34	23	AAU73140	Parathyroid hormon
374	21	67.7	36	15	AAR58201	[Ala10]-hPTH(1-36)
375	21	67.7	36	15	AAR58217	[Ala22]-hPTH(1-36)
376	21	67.7	38	15	AAR58145	[Gly22]-hPTH(1-38)
377	21	67.7	38	15	AAR58146	[Leu22]-hPTH(1-38)
378	21	67.7	38	15	AAR58147	[His22]-hPTH(1-38)
379	21	67.7	38	15	AAR58148	[Ala22]-hPTH(1-38)
380	21	67.7	38	15	AAR58149	[Ile22]-hPTH(1-38)
381	21	67.7	38	15	AAR58150	[Val22]-hPTH(1-38)
382	21	67.7	38	15	AAR58151	[Ser22]-hPTH(1-38)
383	21	67.7	38	15	AAR58152	[Arg22]-hPTH(1-38)
384	20	64.5	34	13	AAR22292	Human parathyroid
385	20	64.5	34	13	AAR22294	Human parathyroid
386	20	64.5	34	13	AAR22296	Human parathyroid
387	20	64.5	34	15	AAR58193	[L8,D10,K11,T33,A3
388	20	64.5	34	15	AAR58194	[A1,H5,L8,D10,K11,
389	20	64.5	34	18	AAW24276	Parathyroid hormon
390	20	64.5	34	18	AAW08108	Human parathyroid
391	20	64.5	34	18	AAW08113	Human PTH derivati
392	20	64.5	34	18	AAW08117	Human PTH derivati

393	20	64.5	34	18	AAW17941	Human parathyroid
394	20	64.5	34	18	AAW17939	Human parathyroid
395	20	64.5	34	19	AAW67274	Parathyroid hormon
396	20	64.5	34	19	AAW67276	Parathyroid hormon
397	20	64.5	34	21	ABJ10713	Human parathyroid
398	20	64.5	34	21	ABJ10737	Human parathyroid
399	20	64.5	34	21	ABJ10769	Human parathyroid
400	20	64.5	34	23	AAU73029	Parathyroid hormon
401	20	64.5	34	23	AAU73030	Parathyroid hormon
402	20	64.5	35	23	AAU73173	Parathyroid hormon
403	20	64.5	36	15	AAR58271	[Ala11]-hPTH(1-36)
404	20	64.5	36	15	AAR58216	[Ala21]-hPTH(1-36)
405	20	64.5	38	15	AAR58138	[Ala21]-hPTH(1-38)
406	20	64.5	38	15	AAR58139	[Gly21]-hPTH(1-38)
407	20	64.5	38	15	AAR58140	[Phe21]-hPTH(1-38)
408	20	64.5	38	15	AAR58141	[Leu21]-hPTH(1-38)
409	20	64.5	38	15	AAR58142	[Asn21]-hPTH(1-38)
410	20	64.5	38	15	AAR58143	[Gln21]-hPTH(1-38)
411	20	64.5	38	15	AAR58144	[Ser21]-hPTH(1-38)
412	19	61.3	28	13	AAR22066	Modified [D-Trp_12
413	19	61.3	30	23	AAU73052	Parathyroid hormon
414	19	61.3	30	23	AAU73053	Parathyroid hormon
415	19	61.3	31	17	AAR88831	Human parathyroid
416	19	61.3	34	11	AAR08300	Human parathyroid
417	19	61.3	34	11	AAR08303	Human parathyroid
418	19	61.3	34	18	AAW08121	Human PTH derivati
419	19	61.3	34	18	AAW08115	Human PTH derivati
420	19	61.3	34	18	AAW08116	Human PTH derivati
421	19	61.3	34	18	AAW17959	Human parathyroid
422	19	61.3	34	22	AAB84771	Parathyroid hormon
423	19	61.3	34	22	AAB84826	Parathyroid hormon
424	19	61.3	34	22	AAB96893	Rat parathyroid ho
425	19	61.3	34	22	AAB96916	Parathyroid hormon
426	19	61.3	34	22	AAB96919	Parathyroid hormon
427	19	61.3	34	22	AAB96930	Rat parathyroid ho
428	19	61.3	35	23	AAU73174	Parathyroid hormon
429	19	61.3	36	15	AAR58279	[Lys20]-hPTH(1-36)
430	19	61.3	36	15	AAR58203	[Ala12]-hPTH(1-36)
431	19	61.3	38	15	AAR58137	[Phe20]-hPTH(1-38)
432	19	61.3	38	15	AAR58089	[Arg12]-hPTH(1-38)
433	19	61.3	38	15	AAR58090	[Ser12]-hPTH(1-38)
434	18	58.1	28	21	AAV98046	Human parathyroid
435	18	58.1	30	6	AAP50665	Human parathyroid
436	18	58.1	30	23	AAU73054	Parathyroid hormon
437	18	58.1	34	13	AAR22297	Human parathyroid
438	18	58.1	34	18	AAW08112	Human PTH derivati
439	18	58.1	34	18	AAW17954	Human parathyroid
440	18	58.1	34	23	AAU73031	Parathyroid hormon
441	18	58.1	35	23	AAU73175	Parathyroid hormon
442	18	58.1	36	15	AAR58204	[Gln13]-hPTH(1-36)
443	18	58.1	36	15	AAR58205	[His13]-hPTH(1-36)
444	18	58.1	36	15	AAR58206	[Leu13]-hPTH(1-36)
445	18	58.1	36	15	AAR58207	[Ala13]-hPTH(1-36)
446	18	58.1	36	15	AAR58214	[Ala19]-hPTH(1-36)
447	18	58.1	38	15	AAR58136	[Arg19]-hPTH(1-38)
448	18	58.1	38	15	AAR58091	[Cys13]-hPTH(1-38)
449	18	58.1	38	15	AAR58092	[Ile13]-hPTH(1-38)

450	18	58.1	38	15	AAR58093	[Asn13]-hPTH(1-38)
451	18	58.1	38	15	AAR58094	[Trp13]-hPTH(1-38)
452	18	58.1	38	15	AAR58095	[Asp13]-hPTH(1-38)
453	18	58.1	38	15	AAR58096	[Val13]-hPTH(1-38)
454	18	58.1	38	15	AAR58097	[Thr13]-hPTH(1-38)
455	18	58.1	38	15	AAR58098	[Ser13]-hPTH(1-38)
456	18	58.1	38	15	AAR58099	[Tyr13]-hPTH(1-38)
457	18	58.1	38	15	AAR58100	[Met13]-hPTH(1-38)
458	18	58.1	38	15	AAR58101	[Gln13]-hPTH(1-38)
459	18	58.1	38	15	AAR58102	[Leu13]-hPTH(1-38)
460	18	58.1	38	15	AAR58103	[Ala13]-hPTH(1-38)
461	18	58.1	38	15	AAR58104	[Gly13]-hPTH(1-38)
462	18	58.1	38	15	AAR58123	[Ser19]-hPTH(1-38)
463	18	58.1	38	15	AAR58124	[Lys19]-hPTH(1-38)
464	18	58.1	38	15	AAR58125	[Leu19]-hPTH(1-38)
465	18	58.1	38	15	AAR58126	[Ala19]-hPTH(1-38)
466	18	58.1	38	15	AAR58127	[Tyr19]-hPTH(1-38)
467	18	58.1	38	15	AAR58128	[Met19]-hPTH(1-38)
468	18	58.1	38	15	AAR58129	[His19]-hPTH(1-38)
469	18	58.1	38	15	AAR58130	[Val19]-hPTH(1-38)
470	18	58.1	38	15	AAR58131	[Gly19]-hPTH(1-38)
471	18	58.1	38	15	AAR58132	[Pro19]-hPTH(1-38)
472	18	58.1	38	15	AAR58133	[Asp19]-hPTH(1-38)
473	18	58.1	38	15	AAR58134	[Ile19]-hPTH(1-38)
474	18	58.1	38	15	AAR58135	[Val19,Gln24]-hPTH
475	17	54.8	28	21	AAV98041	Human parathyroid
476	17	54.8	28	21	AAV98042	Human parathyroid
477	17	54.8	28	21	AAV98044	Human parathyroid
478	17	54.8	31	21	AAV96973	Parathyroid hormone
479	17	54.8	31	21	AAV96974	Parathyroid hormone
480	17	54.8	34	13	AAR22291	Human parathyroid
481	17	54.8	34	18	AAW08129	Human PTH derivati
482	17	54.8	34	19	AAW67298	Parathyroid hormone
483	17	54.8	34	19	AAW67300	Parathyroid hormone
484	17	54.8	34	19	AAW67301	Parathyroid hormone
485	17	54.8	34	19	AAW48394	Human PTH/PTHrP hy
486	17	54.8	34	21	ABJ10742	Human parathyroid
487	17	54.8	34	22	AAB84775	Parathyroid hormone
488	17	54.8	34	22	AAB96922	Parathyroid hormone
489	17	54.8	34	22	AAB91087	Parathyroid hormone
490	17	54.8	36	15	AAR58277	[Nle18]-hPTH(1-36)
491	17	54.8	36	15	AAR58209	[Ala14]-hPTH(1-36)
492	17	54.8	36	15	AAR58183	[Gln18]-hPTH(1-36)
493	17	54.8	36	15	AAR58184	[Tyr18]-hPTH(1-36)
494	17	54.8	36	15	AAR58185	[Lys18]-hPTH(1-36)
495	17	54.8	36	15	AAR58186	[Ala18]-hPTH(1-36)
496	17	54.8	38	15	AAR58037	[Ser14]-hPTH(1-38)
497	17	54.8	38	15	AAR58105	[Val14]-hPTH(1-38)
498	17	54.8	38	15	AAR58106	[Ala14]-hPTH(1-38)
499	17	54.8	38	15	AAR58107	[Lys14]-hPTH(1-38)
500	17	54.8	38	15	AAR58108	[Arg14]-hPTH(1-38)
501	17	54.8	38	15	AAR58109	[Thr14]-hPTH(1-38)
502	17	54.8	38	15	AAR58110	[Ile14]-hPTH(1-38)
503	17	54.8	38	15	AAR58111	[Tyr14]-hPTH(1-38)
504	16	51.6	28	22	AAB81078	Human parathyroid
505	16	51.6	28	23	AAU73105	Parathyroid hormone
506	16	51.6	28	23	AAU73106	Parathyroid hormone

507	16	51.6	31	22	AAB81077	Human parathyroid
508	16	51.6	34	17	AAW14310	Cyclic parathyroid
509	16	51.6	34	17	AAW14311	Cyclic parathyroid
510	16	51.6	34	18	AAW17942	Human parathyroid
511	16	51.6	34	18	AAW17952	Human parathyroid
512	16	51.6	34	18	AAW17958	Human parathyroid
513	16	51.6	34	19	AAW67277	Parathyroid hormon
514	16	51.6	34	19	AAW67287	Parathyroid hormon
515	16	51.6	36	15	AAR58274	[Ala15]-hPTH(1-36)
516	16	51.6	36	15	AAR58212	[Ala17]-hPTH(1-36)
517	16	51.6	38	15	AAR58061	[Ile15]-hPTH(1-38)
518	16	51.6	38	15	AAR58112	[Tyr15]-hPTH(1-38)
519	16	51.6	38	15	AAR58113	[Arg15]-hPTH(1-38)
520	16	51.6	38	15	AAR58114	[Val15]-hPTH(1-38)
521	16	51.6	38	15	AAR58120	[Ala17]-hPTH(1-38)
522	16	51.6	38	15	AAR58121	[Met17]-hPTH(1-38)
523	16	51.6	38	15	AAR58122	[Ile17]-hPTH(1-38)
524	15	48.4	28	13	AAR22058	Modified bovine PT
525	15	48.4	28	13	AAR22059	Modified [Tyr_34]b
526	15	48.4	28	13	AAR22060	Modified [D-Trp_12
527	15	48.4	28	22	AAB91115	Parathyroid hormon
528	15	48.4	28	23	AAE18405	Bovine PTH peptide
529	15	48.4	28	23	AAU73046	Parathyroid hormon
530	15	48.4	28	23	AAU73047	Parathyroid hormon
531	15	48.4	28	23	AAU73050	Parathyroid hormon
532	15	48.4	28	23	AAU73107	Parathyroid hormon
533	15	48.4	28	23	AAU73108	Parathyroid hormon
534	15	48.4	28	23	AAU73109	Parathyroid hormon
535	15	48.4	30	23	AAU73059	Parathyroid hormon
536	15	48.4	31	5	AAP40510	Bovine parathyroid
537	15	48.4	31	21	AAV96975	Parathyroid hormon
538	15	48.4	32	22	AAB91096	Parathyroid hormon
539	15	48.4	32	23	AAE23739	Bovine parathyroid
540	15	48.4	32	23	AAE18402	Bovine PTH peptide
541	15	48.4	32	23	AAU73042	Parathyroid hormon
542	15	48.4	34	11	AAR07918	Bovine parathyroid
543	15	48.4	34	11	AAR07921	Bovine parathyroid
544	15	48.4	34	11	AAR08299	Bovine parathyroid
545	15	48.4	34	11	AAR08302	Bovine parathyroid
546	15	48.4	34	14	AAR41551	[Thr16]hPTH (1-34)
547	15	48.4	34	14	AAR41552	[Glu16]hPTH (1-34)
548	15	48.4	34	14	AAR41553	[Lys16]hPTH (1-34)
549	15	48.4	34	14	AAR41561	[Lys16, Gln27]hPTH
550	15	48.4	34	14	AAR41562	[Orn16, Gln27]hPTH
551	15	48.4	34	14	AAR41563	[Hci16, Gln27]hPTH
552	15	48.4	34	14	AAR41564	[Asp16, Gln27]hPTH
553	15	48.4	34	14	AAR41565	[Arg16, Gln27]hPTH
554	15	48.4	34	14	AAR41571	[D-Lys16]hPTH (1-3
555	15	48.4	34	14	AAR41573	[Gln16]hPTH (1-34)
556	15	48.4	34	14	AAR41574	[Ser16]hPTH (1-34)
557	15	48.4	34	14	AAR41575	[Gly16]hPTH (1-34)
558	15	48.4	34	14	AAR41576	[Lys16]hPTH (1-34)
559	15	48.4	34	14	AAR41577	[Lys16, Asp17]hPTH
560	15	48.4	34	14	AAR41580	[Lys16,17]hPTH (1-
561	15	48.4	34	14	AAR41581	[Arg16,17]hPTH (1-
562	15	48.4	34	17	AAR99979	Bovine parathyroid
563	15	48.4	34	17	AAR99981	Porcine parathyroi

564	15	48.4	34	18	AAW08124	Human PTH derivati
565	15	48.4	34	18	AAW08132	Human PTH derivati
566	15	48.4	34	18	AAW08111	Human PTH derivati
567	15	48.4	34	18	AAW19995	Cyclised bovine pa
568	15	48.4	34	18	AAW20001	Cyclised bovine pa
569	15	48.4	34	18	AAW20007	Cyclised bovine pa
570	15	48.4	34	18	AAW17967	Human PTH analogue
571	15	48.4	34	18	AAW17953	Human parathyroid
572	15	48.4	34	18	AAW17956	Human parathyroid
573	15	48.4	34	18	AAW17963	Human PTH analogue
574	15	48.4	34	19	AAW61659	Parathyroid hormon
575	15	48.4	34	19	AAW61660	Parathyroid hormon
576	15	48.4	34	19	AAW65976	Bovine parathyroid
577	15	48.4	34	19	AAW65977	Porcine parathyroi
578	15	48.4	34	19	AAW42615	Bovine parathyroid
579	15	48.4	34	19	AAW42616	Porcine parathyroi
580	15	48.4	34	20	AAW81872	Bovine PTH N-termi
581	15	48.4	34	20	AAW81873	Porcine PTH N-term
582	15	48.4	34	23	AAE23738	Bovine parathyroid
583	15	48.4	34	23	AAE18394	Bovine PTH peptide
584	15	48.4	34	23	AAU73034	Parathyroid hormon
585	15	48.4	34	23	AAU73036	Parathyroid hormon
586	15	48.4	36	15	AAR58275	[Ala16]-hPTH(1-36)
587	15	48.4	37	22	AAB86230	Bovine parathyroid
588	15	48.4	37	22	AAB86232	Porcine parathyroi
589	15	48.4	37	22	AAB86233	Canine parathyroid
590	15	48.4	37	23	ABB82204	Bovine parathyroid
591	15	48.4	38	15	AAR58036	[Gln16]-hPTH(1-38)
592	15	48.4	38	15	AAR58115	[Lys16]-hPTH(1-38)
593	15	48.4	38	15	AAR58116	[Ser16]-hPTH(1-38)
594	15	48.4	38	15	AAR58117	[Leu16]-hPTH(1-38)
595	15	48.4	38	15	AAR58118	[Ala16]-hPTH(1-38)
596	15	48.4	38	15	AAR58119	[Gly16]-hPTH(1-38)
597	14	45.2	28	23	AAU73066	Parathyroid hormon
598	14	45.2	30	23	AAU73057	Parathyroid hormon
599	14	45.2	30	23	AAU73060	Parathyroid hormon
600	14	45.2	34	9	AAP82177	Sequence of parath
601	14	45.2	34	11	AAR07917	Rat parathyroid ho
602	14	45.2	34	11	AAR07920	Rat parathyroid ho
603	14	45.2	34	14	AAR41568	[Lys15,16 His27]hP
604	14	45.2	34	14	AAR41569	[Lys15, His27]hPTH
605	14	45.2	34	14	AAR41572	[Lys15,16,17, His2
606	14	45.2	34	14	AAR41578	[Lys14,15,16,17]hP
607	14	45.2	34	14	AAR41579	[Lys15,15,17]hPTH
608	14	45.2	34	14	AAR41582	[Arg15,16,17]hPTH
609	14	45.2	34	16	AAR62432	Accelerator peptid
610	14	45.2	34	17	AAW14308	Cyclic parathyroid
611	14	45.2	34	17	AAW14309	Cyclic parathyroid
612	14	45.2	34	17	AAW14312	Cyclic parathyroid
613	14	45.2	34	17	AAW14313	Cyclic parathyroid
614	14	45.2	34	17	AAW14314	Cyclic parathyroid
615	14	45.2	34	17	AAW14315	Cyclic parathyroid
616	14	45.2	34	17	AAR99980	Rat parathyroid ho
617	14	45.2	34	18	AAW08122	Human PTH derivati
618	14	45.2	34	18	AAW08123	Human PTH derivati
619	14	45.2	34	18	AAW19996	Cyclised rat parat
620	14	45.2	34	18	AAW20002	Cyclised rat parat

621	14	45.2	34	18	AAW20008	Cyclised rat parat
622	14	45.2	34	19	AAW48398	Human PTH/PTHrP hy
623	14	45.2	34	22	AAB84777	Native human parat
624	14	45.2	34	22	AAB96897	Rat parathyroid ho
625	14	45.2	34	22	AAB91100	Parathyroid hormon
626	14	45.2	34	23	AAU73037	Parathyroid hormon
627	14	45.2	34	24	ABP71489	Parathyroid hormon
628	14	45.2	34	24	ABP71499	Rat parathyroid ho
629	14	45.2	36	15	AAR58071	[Aib3, Gln18]-hPTH
630	14	45.2	36	15	AAR58088	[1-amino-cyclopent
631	14	45.2	37	22	AAB86231	Rat parathyroid ho
632	13	41.9	28	13	AAR22061	Modified [Nle ₈ ,18
633	13	41.9	28	13	AAR22062	Modified [Nle ₈ ,18
634	13	41.9	28	13	AAR22067	Modified [Nle ₈ ,_1
635	13	41.9	28	13	AAR22068	Modified [Nle ₈ ,_1
636	13	41.9	28	21	ABJ10774	Human parathyroid
637	13	41.9	28	21	ABJ10775	Human parathyroid
638	13	41.9	28	23	AAE18404	Bovine PTH peptide
639	13	41.9	28	23	AAU73045	Parathyroid hormon
640	13	41.9	28	23	AAU73048	Parathyroid hormon
641	13	41.9	28	23	AAU73049	Parathyroid hormon
642	13	41.9	30	22	AAB91089	Parathyroid hormon
643	13	41.9	30	22	AAB91092	Parathyroid hormon
644	13	41.9	31	5	AAP40511	Bovine parathyroid
645	13	41.9	31	5	AAP40761	Human parathyroid
646	13	41.9	32	22	AAB91088	Parathyroid hormon
647	13	41.9	32	22	AAB91090	Parathyroid hormon
648	13	41.9	32	22	AAB91091	Parathyroid hormon
649	13	41.9	32	23	AAE18403	Bovine PTH peptide
650	13	41.9	32	23	AAU73041	Parathyroid hormon
651	13	41.9	32	23	AAU73043	Parathyroid hormon
652	13	41.9	33	17	AAW15814	[Leu(8),Trp(10),Al
653	13	41.9	34	6	AAP50517	Sequence of methio
654	13	41.9	34	11	AAR07924	Bovine parathyroid
655	13	41.9	34	11	AAR07925	Human parathyroid
656	13	41.9	34	11	AAR08305	Bovine parathyroid
657	13	41.9	34	11	AAR08306	Human parathyroid
658	13	41.9	34	13	AAR22295	Human parathyroid
659	13	41.9	34	15	AAR45528	Parathyroid hormon
660	13	41.9	34	15	AAR58239	Isopropyl-[Nle ₈ ,18
661	13	41.9	34	15	AAR58241	[Nle ₈ ,18,D-Asn33,D
662	13	41.9	34	15	AAR58195	[S14,I15,Q16,D17,L
663	13	41.9	34	15	AAR55817	[L8,Q18,T33,A34]-h
664	13	41.9	34	15	AAR55819	[L8,A16,Q18,T33,A3
665	13	41.9	34	15	AAR55821	[L8,D10,K11,Q18,T3
666	13	41.9	34	15	AAR55823	[L8,D10,K11,A16,Q1
667	13	41.9	34	15	AAR58021	[L8,D10,A16,Q18,T3
668	13	41.9	34	15	AAR58034	Isopropyl-[L8,K(Is
669	13	41.9	34	16	AAR69055	PTH analogue with
670	13	41.9	34	17	AAW15813	[Leu(8),Trp(10),Al
671	13	41.9	34	17	AAW15815	[Leu(8),Trp(10),DL
672	13	41.9	34	17	AAW15828	N-alpha-acylated [
673	13	41.9	34	17	AAW14316	Cyclic parathyroid
674	13	41.9	34	18	AAW13352	Truncated parathyr
675	13	41.9	34	18	AAW12651	Parathyroid hormon
676	13	41.9	34	18	AAW20004	Cyclised [Nle ₈ ,18
677	13	41.9	34	18	AAW19997	Cyclised [Nle ₈ ,18

678	13	41.9	34	18	AAW19998	Cyclised [Nle 8,18
679	13	41.9	34	18	AAW20003	Cyclised [Nle 8,18
680	13	41.9	34	18	AAW20009	Cyclised [Nle 8,18
681	13	41.9	34	18	AAW20010	Cyclised [Nle 8,18
682	13	41.9	34	18	AAW17940	Human PTH analogue
683	13	41.9	34	18	AAW17970	Human PTH analogue
684	13	41.9	34	18	AAW17964	Human PTH analogue
685	13	41.9	34	19	AAW67275	Parathyroid hormon
686	13	41.9	34	19	AAW61725	Parathyroid hormon
687	13	41.9	34	19	AAW66053	Parathyroid hormon
688	13	41.9	34	19	AAW42602	Parathyroid hormon
689	13	41.9	34	19	AAW48395	Human PTH/PTHrP hy
690	13	41.9	34	20	AAW02587	Parathyroid hormon
691	13	41.9	34	20	AAW92218	Analogue of parath
692	13	41.9	34	20	AAW92219	Analogue of parath
693	13	41.9	34	20	AAW03920	Analogue of parath
694	13	41.9	34	20	AAW03921	Analogue of parath
695	13	41.9	34	20	AAW03922	Analogue of parath
696	13	41.9	34	20	AAW03923	Analogue of parath
697	13	41.9	34	20	AAW03924	Analogue of parath
698	13	41.9	34	20	AAW03925	Analogue of parath
699	13	41.9	34	20	AAW03926	Analogue of parath
700	13	41.9	34	20	AAW03927	Analogue of parath
701	13	41.9	34	20	AAW03928	Analogue of parath
702	13	41.9	34	20	AAW03929	Analogue of parath
703	13	41.9	34	20	AAW03930	Analogue of parath
704	13	41.9	34	20	AAW03931	Analogue of parath
705	13	41.9	34	20	AAW03932	Analogue of parath
706	13	41.9	34	20	AAW03933	Analogue of parath
707	13	41.9	34	20	AAW92236	Analogue of parath
708	13	41.9	34	20	AAW92237	Analogue of parath
709	13	41.9	34	20	AAW92238	Analogue of parath
710	13	41.9	34	20	AAW92239	Analogue of parath
711	13	41.9	34	20	AAW92240	Analogue of parath
712	13	41.9	34	20	AAW92241	Analogue of parath
713	13	41.9	34	20	AAW92242	Analogue of parath
714	13	41.9	34	20	AAW92243	Analogue of parath
715	13	41.9	34	20	AAW92244	Analogue of parath
716	13	41.9	34	20	AAW92245	Analogue of parath
717	13	41.9	34	20	AAW92246	Analogue of parath
718	13	41.9	34	20	AAW92247	Analogue of parath
719	13	41.9	34	20	AAW92248	Analogue of parath
720	13	41.9	34	20	AAW92249	Analogue of parath
721	13	41.9	34	20	AAW92250	Analogue of parath
722	13	41.9	34	20	AAW03919	Analogue of parath
723	13	41.9	34	20	AAW92220	Analogue of parath
724	13	41.9	34	20	AAW92221	Analogue of parath
725	13	41.9	34	20	AAW92222	Analogue of parath
726	13	41.9	34	20	AAW92223	Analogue of parath
727	13	41.9	34	20	AAW92224	Analogue of parath
728	13	41.9	34	20	AAW92225	Analogue of parath
729	13	41.9	34	20	AAW92226	Analogue of parath
730	13	41.9	34	20	AAW92227	Analogue of parath
731	13	41.9	34	20	AAW92228	Analogue of parath
732	13	41.9	34	20	AAW92229	Analogue of parath
733	13	41.9	34	20	AAW92230	Analogue of parath
734	13	41.9	34	20	AAW92231	Analogue of parath

735	13	41.9	34	20	AAW92232	Analogue of parath
736	13	41.9	34	20	AAW92233	Analogue of parath
737	13	41.9	34	20	AAW92234	Analogue of parath
738	13	41.9	34	20	AAW92235	Analogue of parath
739	13	41.9	34	20	AAW92236	Analogue of parath
740	13	41.9	34	20	AAW92237	Analogue of parath
741	13	41.9	34	20	AAW92238	Analogue of parath
742	13	41.9	34	20	AAW92239	Analogue of parath
743	13	41.9	34	20	AAW92240	Analogue of parath
744	13	41.9	34	20	AAW92241	Analogue of parath
745	13	41.9	34	20	AAW92242	Analogue of parath
746	13	41.9	34	20	AAW92243	Analogue of parath
747	13	41.9	34	20	AAW92244	Analogue of parath
748	13	41.9	34	20	AAW92245	Analogue of parath
749	13	41.9	34	20	AAW92246	Analogue of parath
750	13	41.9	34	20	AAW92247	Analogue of parath
751	13	41.9	34	20	AAW92248	Analogue of parath
752	13	41.9	34	20	AAW92249	Analogue of parath
753	13	41.9	34	20	AAW92250	Analogue of parath
754	13	41.9	34	20	AAW92251	Analogue of parath
755	13	41.9	34	20	AAW92252	Analogue of parath
756	13	41.9	34	20	AAW92253	Analogue of parath
757	13	41.9	34	20	AAW92254	Analogue of parath
758	13	41.9	34	20	AAW92255	Analogue of parath
759	13	41.9	34	20	AAW92256	Analogue of parath
760	13	41.9	34	20	AAW92257	Analogue of parath
761	13	41.9	34	20	AAW92258	Analogue of parath
762	13	41.9	34	20	AAW92259	Analogue of parath
763	13	41.9	34	20	AAW92260	Analogue of parath
764	13	41.9	34	20	AAW92261	Analogue of parath
765	13	41.9	34	20	AAW92262	Analogue of parath
766	13	41.9	34	20	AAW92263	Analogue of parath
767	13	41.9	34	20	AAW92264	Analogue of parath
768	13	41.9	34	20	AAW92265	Analogue of parath
769	13	41.9	34	20	AAW92266	Analogue of parath
770	13	41.9	34	20	AAW92267	Analogue of parath
771	13	41.9	34	20	AAW92268	Analogue of parath
772	13	41.9	34	20	AAW92269	Analogue of parath
773	13	41.9	34	20	AAW92270	Analogue of parath
774	13	41.9	34	20	AAW92271	Analogue of parath
775	13	41.9	34	20	AAW92272	Analogue of parath
776	13	41.9	34	20	AAW92273	Analogue of parath
777	13	41.9	34	20	AAW92274	Analogue of parath
778	13	41.9	34	20	AAW92275	Analogue of parath
779	13	41.9	34	20	AAW92276	Analogue of parath
780	13	41.9	34	20	AAW92277	Analogue of parath
781	13	41.9	34	20	AAW92278	Analogue of parath
782	13	41.9	34	20	AAW92279	Analogue of parath
783	13	41.9	34	20	AAW92280	Analogue of parath
784	13	41.9	34	20	AAW92281	Analogue of parath
785	13	41.9	34	20	AAW92282	Analogue of parath
786	13	41.9	34	20	AAW92283	Analogue of parath
787	13	41.9	34	20	AAW92284	Analogue of parath
788	13	41.9	34	20	AAW92285	Analogue of parath
789	13	41.9	34	20	AAW92286	Analogue of parath
790	13	41.9	34	20	AAW92287	Analogue of parath
791	13	41.9	34	20	AAW92288	Analogue of parath

792	13	41.9	34	20	AAW92192	Analogue of parath
793	13	41.9	34	20	AAW92193	Analogue of parath
794	13	41.9	34	20	AAW92194	Analogue of parath
795	13	41.9	34	20	AAW92195	Analogue of parath
796	13	41.9	34	20	AAW92196	Analogue of parath
797	13	41.9	34	20	AAW92197	Analogue of parath
798	13	41.9	34	20	AAW92166	Analogue of parath
799	13	41.9	34	20	AAW92168	Analogue of parath
800	13	41.9	34	20	AAW92169	Analogue of parath
801	13	41.9	34	20	AAW92170	Analogue of parath
802	13	41.9	34	20	AAW92171	Analogue of parath
803	13	41.9	34	20	AAW92172	Analogue of parath
804	13	41.9	34	20	AAW92173	Analogue of parath
805	13	41.9	34	20	AAW92174	Analogue of parath
806	13	41.9	34	20	AAW92175	Analogue of parath
807	13	41.9	34	20	AAW92176	Analogue of parath
808	13	41.9	34	20	AAW92177	Analogue of parath
809	13	41.9	34	20	AAW92178	Analogue of parath
810	13	41.9	34	20	AAW92179	Analogue of parath
811	13	41.9	34	20	AAW92180	Analogue of parath
812	13	41.9	34	20	AAW92181	Analogue of parath
813	13	41.9	34	20	AAW92182	Analogue of parath
814	13	41.9	34	20	AAW92152	Analogue of parath
815	13	41.9	34	20	AAW92150	Analogue of parath
816	13	41.9	34	20	AAW92151	Analogue of parath
817	13	41.9	34	20	AAW92153	Analogue of parath
818	13	41.9	34	20	AAW92154	Analogue of parath
819	13	41.9	34	20	AAW92155	Analogue of parath
820	13	41.9	34	20	AAW92156	Analogue of parath
821	13	41.9	34	20	AAW92157	Analogue of parath
822	13	41.9	34	20	AAW92158	Analogue of parath
823	13	41.9	34	20	AAW92159	Analogue of parath
824	13	41.9	34	20	AAW92160	Analogue of parath
825	13	41.9	34	20	AAW92161	Analogue of parath
826	13	41.9	34	20	AAW92162	Analogue of parath
827	13	41.9	34	20	AAW92163	Analogue of parath
828	13	41.9	34	20	AAW92164	Analogue of parath
829	13	41.9	34	20	AAW92165	Analogue of parath
830	13	41.9	34	20	AAW92148	Analogue of parath
831	13	41.9	34	20	AAW92149	Analogue of parath
832	13	41.9	34	20	AAW74396	Modified parathyro
833	13	41.9	34	20	AAW81945	Synthetic PTH and
834	13	41.9	34	21	ABJ10705	Human parathyroid
835	13	41.9	34	21	ABJ10707	Human parathyroid
836	13	41.9	34	21	ABJ10708	Human parathyroid
837	13	41.9	34	21	ABJ10709	Human parathyroid
838	13	41.9	34	21	ABJ10710	Human parathyroid
839	13	41.9	34	21	ABJ10711	Human parathyroid
840	13	41.9	34	21	ABJ10715	Human parathyroid
841	13	41.9	34	21	ABJ10716	Human parathyroid
842	13	41.9	34	21	ABJ10718	Human parathyroid
843	13	41.9	34	21	ABJ10720	Human parathyroid
844	13	41.9	34	21	ABJ10721	Human parathyroid
845	13	41.9	34	21	ABJ10723	Human parathyroid
846	13	41.9	34	21	ABJ10725	Human parathyroid
847	13	41.9	34	21	ABJ10726	Human parathyroid
848	13	41.9	34	21	ABJ10728	Human parathyroid

849	13	41.9	34	21	ABJ10731	Human parathyroid
850	13	41.9	34	21	ABJ10732	Human parathyroid
851	13	41.9	34	21	ABJ10734	Human parathyroid
852	13	41.9	34	21	ABJ10735	Human parathyroid
853	13	41.9	34	21	ABJ10738	Human parathyroid
854	13	41.9	34	21	ABJ10739	Human parathyroid
855	13	41.9	34	21	ABJ10740	Human parathyroid
856	13	41.9	34	21	ABJ10741	Human parathyroid
857	13	41.9	34	21	ABJ10743	Human parathyroid
858	13	41.9	34	21	ABJ10744	Human parathyroid
859	13	41.9	34	21	ABJ10745	Human parathyroid
860	13	41.9	34	21	ABJ10746	Human parathyroid
861	13	41.9	34	21	ABJ10747	Human parathyroid
862	13	41.9	34	21	ABJ10748	Human parathyroid
863	13	41.9	34	21	ABJ10749	Human parathyroid
864	13	41.9	34	21	ABJ10750	Human parathyroid
865	13	41.9	34	21	ABJ10751	Human parathyroid
866	13	41.9	34	21	ABJ10752	Human parathyroid
867	13	41.9	34	21	ABJ10753	Human parathyroid
868	13	41.9	34	21	ABJ10754	Human parathyroid
869	13	41.9	34	21	ABJ10755	Human parathyroid
870	13	41.9	34	21	ABJ10756	Human parathyroid
871	13	41.9	34	21	ABJ10761	Human parathyroid
872	13	41.9	34	21	ABJ10762	Human parathyroid
873	13	41.9	34	21	ABJ10763	Human parathyroid
874	13	41.9	34	21	ABJ10764	Human parathyroid
875	13	41.9	34	21	ABJ10765	Human parathyroid
876	13	41.9	34	21	ABJ10766	Human parathyroid
877	13	41.9	34	21	ABJ10767	Human parathyroid
878	13	41.9	34	21	ABJ10768	Human parathyroid
879	13	41.9	34	21	ABJ10771	Human parathyroid
880	13	41.9	34	21	ABJ10777	Human parathyroid
881	13	41.9	34	22	AAB91084	Parathyroid hormon
882	13	41.9	34	23	AAE18396	Bovine PTH peptide
883	13	41.9	34	23	AAE18397	Human PTH peptide
884	13	41.9	34	23	AAU73033	Parathyroid hormon
885	13	41.9	34	23	AAU73035	Parathyroid hormon
886	13	41.9	35	2	AAP10140	h-PTH antigen. Sy
887	13	41.9	35	16	AAR74512	Parathyroid hormon
888	13	41.9	35	16	AAR74513	Parathyroid hormon
889	13	41.9	35	16	AAR74514	Parathyroid hormon
890	13	41.9	35	16	AAR74515	Parathyroid hormon
891	13	41.9	35	16	AAR74516	Parathyroid hormon
892	13	41.9	35	16	AAR74517	Parathyroid hormon
893	13	41.9	35	16	AAR74518	Parathyroid hormon
894	13	41.9	35	16	AAR74519	Parathyroid hormon
895	13	41.9	35	16	AAR74520	Parathyroid hormon
896	13	41.9	35	16	AAR74527	Human parathyroid
897	13	41.9	35	16	AAR74511	Parathyroid hormon
898	13	41.9	35	16	AAR74464	Parathyroid hormon
899	13	41.9	35	16	AAR74465	Parathyroid hormon
900	13	41.9	35	16	AAR74466	Parathyroid hormon
901	13	41.9	35	16	AAR74467	Parathyroid hormon
902	13	41.9	35	16	AAR74468	Parathyroid hormon
903	13	41.9	35	16	AAR74469	Parathyroid hormon
904	13	41.9	35	16	AAR74470	Parathyroid hormon
905	13	41.9	35	16	AAR74471	Parathyroid hormon

906	13	41.9	35	16	AAR74472	Parathyroid hormon
907	13	41.9	35	16	AAR74473	Parathyroid hormon
908	13	41.9	35	16	AAR74474	Parathyroid hormon
909	13	41.9	35	16	AAR74475	Parathyroid hormon
910	13	41.9	35	16	AAR74476	Parathyroid hormon
911	13	41.9	35	16	AAR74477	Parathyroid hormon
912	13	41.9	35	16	AAR74478	Parathyroid hormon
913	13	41.9	35	16	AAR74479	Parathyroid hormon
914	13	41.9	35	16	AAR74448	Parathyroid hormon
915	13	41.9	35	16	AAR74449	Parathyroid hormon
916	13	41.9	35	16	AAR74450	Parathyroid hormon
917	13	41.9	35	16	AAR74451	Parathyroid hormon
918	13	41.9	35	16	AAR74452	Parathyroid hormon
919	13	41.9	35	16	AAR74453	Parathyroid hormon
920	13	41.9	35	16	AAR74454	Parathyroid hormon
921	13	41.9	35	16	AAR74455	Parathyroid hormon
922	13	41.9	35	16	AAR74456	Parathyroid hormon
923	13	41.9	35	16	AAR74457	Parathyroid hormon
924	13	41.9	35	16	AAR74458	Parathyroid hormon
925	13	41.9	35	16	AAR74459	Parathyroid hormon
926	13	41.9	35	16	AAR74460	Parathyroid hormon
927	13	41.9	35	16	AAR74461	Parathyroid hormon
928	13	41.9	35	16	AAR74462	Parathyroid hormon
929	13	41.9	35	16	AAR74463	Parathyroid hormon
930	13	41.9	35	16	AAR74432	Parathyroid hormon
931	13	41.9	35	16	AAR74433	Parathyroid hormon
932	13	41.9	35	16	AAR74434	Parathyroid hormon
933	13	41.9	35	16	AAR74435	Parathyroid hormon
934	13	41.9	35	16	AAR74436	Parathyroid hormon
935	13	41.9	35	16	AAR74437	Parathyroid hormon
936	13	41.9	35	16	AAR74438	Parathyroid hormon
937	13	41.9	35	16	AAR74439	Parathyroid hormon
938	13	41.9	35	16	AAR74440	Parathyroid hormon
939	13	41.9	35	16	AAR74441	Parathyroid hormon
940	13	41.9	35	16	AAR74442	Parathyroid hormon
941	13	41.9	35	16	AAR74443	Parathyroid hormon
942	13	41.9	35	16	AAR74444	Parathyroid hormon
943	13	41.9	35	16	AAR74445	Parathyroid hormon
944	13	41.9	35	16	AAR74446	Parathyroid hormon
945	13	41.9	35	16	AAR74447	Parathyroid hormon
946	13	41.9	35	16	AAR74429	Parathyroid hormon
947	13	41.9	35	16	AAR74430	Parathyroid hormon
948	13	41.9	35	16	AAR74431	Parathyroid hormon
949	13	41.9	35	16	AAR74398	Parathyroid hormon
950	13	41.9	35	16	AAR74399	Parathyroid hormon
951	13	41.9	35	16	AAR74400	Parathyroid hormon
952	13	41.9	35	16	AAR74408	Parathyroid hormon
953	13	41.9	35	16	AAR74409	Parathyroid hormon
954	13	41.9	35	16	AAR74394	Parathyroid hormon
955	13	41.9	35	16	AAR74395	Parathyroid hormon
956	13	41.9	35	16	AAR74396	Parathyroid hormon
957	13	41.9	35	16	AAR74397	Parathyroid hormon
958	13	41.9	36	15	AAR58042	[L8,D10,K11,L18] -h
959	13	41.9	36	15	AAR58044	[L8,D10,K11,A17,L1
960	13	41.9	36	15	AAR58055	[L8,Q18] -hPTH(1-36
961	13	41.9	36	15	AAR58057	[L8,D10,A16,Q18] -h
962	13	41.9	36	15	AAR55820	[L8,D10,K11,Q18] -h

963	13	41.9	36	15	AAR55824	[L8,D10,K11,A16,Q1
964	13	41.9	36	15	AAR58027	[A1,A3,L8,Q18]-hPT
965	13	41.9	36	15	AAR58031	[L8,K11,Q18]-hPTH(
966	13	41.9	36	15	AAR58072	Isopropyl-[L8,D10,
967	13	41.9	36	15	AAR58074	[L8,Y18]-hPTH(1-36
968	12	38.7	28	23	AAU73065	Parathyroid hormon
969	12	38.7	28	23	AAU73067	Parathyroid hormon
970	12	38.7	30	23	AAU73056	Parathyroid hormon
971	12	38.7	30	23	AAU73058	Parathyroid hormon
972	12	38.7	32	22	AAB84835	Parathyroid hormon
973	12	38.7	32	22	AAB96906	Parathyroid hormon
974	12	38.7	34	14	AAV18002	Human PTH(1-34) de
975	12	38.7	34	15	AAR58045	[L8,Q16,D17,L18,R1
976	12	38.7	34	15	AAR58049	[L8,D10,K11,Q16,D1
977	12	38.7	34	15	AAR58056	[L8,D10,K11,A16,Q1
978	12	38.7	34	15	AAR58058	[L8,D10,K11,A16,Q1
979	12	38.7	34	15	AAR55818	[L8,A16,Q18,A19,T3
980	12	38.7	34	18	AAW08130	Human PTH derivati
981	12	38.7	34	18	AAW17960	Human PTH analogue
982	12	38.7	34	18	AAW17962	Human PTH analogue
983	12	38.7	34	21	ABJ10757	Human parathyroid
984	12	38.7	34	21	ABJ10770	Human parathyroid
985	12	38.7	34	22	AAB84828	Parathyroid hormon
986	12	38.7	34	22	AAB96921	Parathyroid hormon
987	12	38.7	34	24	ABP71490	Parathyroid hormon
988	12	38.7	34	24	ABP71491	Parathyroid hormon
989	12	38.7	34	24	ABP71492	Parathyroid hormon
990	12	38.7	34	24	ABP71494	Parathyroid hormon
991	12	38.7	35	16	AAR74507	Parathyroid hormon
992	12	38.7	35	16	AAR74508	Parathyroid hormon
993	12	38.7	35	16	AAR74509	Parathyroid hormon
994	12	38.7	35	16	AAR74510	Parathyroid hormon
995	12	38.7	35	16	AAR74480	Parathyroid hormon
996	12	38.7	35	16	AAR74401	Parathyroid hormon
997	12	38.7	35	16	AAR74412	Parathyroid hormon
998	12	38.7	36	15	AAR58208	[A13,Q26,F27,D-F34
999	12	38.7	36	15	AAR58041	[L8,D10,K11,S14,I1
1000	12	38.7	36	15	AAR58043	[L8,Q16,D17,L18,R1

ALIGNMENTS

RESULT 1

AAW42059

ID AAW42059 standard; peptide; 31 AA.

XX

AC AAW42059;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:14.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 22
FT /note= "Glu is bound to Lys at position 26 to form
FT a cyclic structure"
FT Modified-site 26
FT /note= "Lys is bound to Glu at position 22 to form
FT a cyclic structure"
FT Modified-site 31
FT /note= "amidated"
XX
PN WO9805683-A1.
XX
PD 12-FEB-1998.
XX
PF 01-AUG-1997; 97WO-CA00547.
XX
PR 14-MAR-1997; 97US-0040560.
PR 02-AUG-1996; 96US-0691647.
XX
PA (CANA) NAT RES COUNCIL CANADA.
XX
PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
PI Willick GE;
XX
DR WPI; 1998-145550/13.
XX
PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
PT - for treating osteoporosis and fractures, also method for screening
PT osteogenic peptide(s) based on their hypotensive action
XX
PS Claim 41; Fig 21; 77pp; English.
XX
CC The present sequence represents a human parathyroid hormone (hPTH)
CC (1-31) peptide analogue. The present invention also describes a method
CC for screening peptides for osteogenic activity by subcutaneous injection
CC of a test compound and seeing if a small drop in arterial pressure
CC occurs after a short time. The hPTH peptide analogue can be useful for
CC stimulating bone growth, restoring bone and promoting bone healing,
CC especially treatment of osteoporosis and normal fractures. The hPTH
CC peptide analogue can be administered by injection or inhalation,
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 31; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.1e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Db |||||
1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 2

AAW42051

ID AAW42051 standard; peptide; 31 AA.

XX

AC AAW42051;

XX

DT 06-JUL-1998 (first entry)

XX

DE Human parathyroid hormone cyclic peptide analogue SEQ ID NO:6.

XX

KW Human; parathyroid hormone; hPTH; cyclic; osteoporosis; fracture;
KW hypotensive action; bone.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 27

FT /note= "Lys is bound to Asp at position 30 to form
FT a cyclic structure"

FT Modified-site 30

FT /note= "Asp is bound to Lys at position 27 to form
FT a cyclic structure"

FT Modified-site 31

FT /note= "amidated"

XX

PN WO9805683-A1.

XX

PD 12-FEB-1998.

XX

PF 01-AUG-1997; 97WO-CA00547.

XX

PR 14-MAR-1997; 97US-0040560.

PR 02-AUG-1996; 96US-0691647.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Neugebauer W, Ross V, Whitfield J;
PI Willick GE;

XX

DR WPI; 1998-145550/13.

XX

PT Cyclic human parathyroid hormone peptide(s) with 27Lys substitution
PT - for treating osteoporosis and fractures, also method for screening
PT osteogenic peptide(s) based on their hypotensive action

XX

PS Claim 33; Fig 10; 77pp; English.

XX

CC The present sequence represents a human parathyroid hormone (hPTH)
CC (1-31) peptide analogue. The present invention also describes a method
CC for screening peptides for osteogenic activity by subcutaneous injection
CC of a test compound and seeing if a small drop in arterial pressure
CC occurs after a short time. The hPTH peptide analogue can be useful for

CC stimulating bone growth, restoring bone and promoting bone healing,
CC especially treatment of osteoporosis and normal fractures. The hPTH
CC peptide analogue can be administered by injection or inhalation,
CC rectally or orally, generally at at most 0.05 mg/kg/day. Substitution
CC of Lys26 stabilises an alpha-helix in the receptor-binding region of
CC the hormone and increases adenylyl cyclase (AC) activity, while
CC cyclisation increases stability against proteases. The screening method,
CC which can be performed in intact female animals, is a quick and simple
CC way of identifying inactive compounds, avoiding the need for long-term,
CC expensive tests on ovariectomised animals.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 31; DB 19; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.1e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 3

AAY02578

ID AAY02578 standard; peptide; 31 AA.

XX

AC AAY02578;

XX

DT 16-JUL-1999 (first entry)

XX

DE N-terminal 31 residues of human parathyroid hormone (hPTH).

XX

KW Human parathyroid hormone; hPTH; bone mass;

KW 3-(substituted phenoxy)benzo(b)thiophene compound;

KW bone loss treatment; osteoporosis.

XX

OS Homo sapiens.

XX

PN WO9918945-A1.

XX

PD 22-APR-1999.

XX

PF 05-OCT-1998; 98WO-US20848.

XX

PR 14-OCT-1997; 97US-0061800.

XX

PA (ELIL) LILLY & CO ELI.

XX

PI Sato M;

XX

DR WPI; 1999-287871/24.

XX

PT Method of building bone mass by co-administration of a parathyroid

PT hormone with a 3-(substituted phenoxy)benzo(b)thiophene compound

XX

PS Claim 6; Page 39; 48pp; English.

XX

CC The present sequence represents a fragment of human parathyroid hormone
CC (hPTH). hPTH and its fragments are used in the method of the invention.
CC The specification describes a method for building bone mass, comprising
CC coadministration of a parathyroid hormone with a 3-(substituted
CC phenoxy)benzo(b)thiophene compound. The method is used for treatment
CC of bone loss, e.g. in osteoporosis.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 31; DB 20; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.1e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 4

AAB81080

ID AAB81080 standard; peptide; 31 AA.

XX

AC AAB81080;

XX

DT 26-JUN-2001 (first entry)

XX

DE Human parathyroid hormone 1-31.

XX

KW Parathyroid hormone; PTH; blood calcium level regulator; osteopathic;
KW vulnerary; bone growth; bone healing; osteoporosis; fracture; human.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 31

FT /note= "C-terminal amide"

XX

PN WO200121643-A2.

XX

PD 29-MAR-2001.

XX

PF 21-SEP-2000; 2000WO-CA01083.

XX

PR 22-SEP-1999; 99US-0406813.

XX

PA (CANA) NAT RES COUNCIL CANADA.

XX

PI Barbier J, Morley P, Whitfield J, Willick GE;

XX

DR WPI; 2001-308081/32.

XX

PT New human parathyroid hormone (HPTH) analog useful for stimulating bone
PT growth, for restoring bone, for promotion of bone healing, and for
PT treating osteoporosis and normal fractures -

XX

PS Disclosure; Fig 2; 34pp; English.

XX

XX
 CC The present invention describes a modified therapeutic peptide (I)
 CC comprising a therapeutically active amino acid region (III) and a
 CC reactive group (II) (e.g. succinimidyl and maleimido groups) attached to
 CC a less therapeutically active amino acid region (IV), which covalently
 CC bonds with amino/hydroxyl/thiol groups on blood components to form a
 CC peptidase stabilised therapeutic peptide composed of 3-50 amino acids.
 CC (I) are useful for modifying therapeutic peptides e.g. hormones, growth
 CC factors and neurotransmitters, to protect them from peptidase activity
 CC in vivo for the treatment of various disorders. Endogenous therapeutic
 CC peptides are not suitable as drug candidates as they require frequent
 CC administration due to rapid degradation by peptidases in the body.
 CC Modifying and attaching therapeutic peptides to albumin prevents or
 CC reduces the action of peptidases to increase length of activity (half
 CC life) and specificity as bonding to large molecules decreases
 CC intracellular uptake and interference with physiological processes.
 CC AAB90829 to AAB92441 represent peptides which can be used in the
 CC exemplification of the present invention.

XX

SQ Sequence 31 AA;

Query Match 100.0%; Score 31; DB 22; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.1e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 6

AAE23720

ID AAE23720 standard; peptide; 31 AA.

XX

AC AAE23720;

XX

DT 10-SEP-2002 (first entry)

XX

DE Human parathyroid hormone (hPTH) peptide (1-31).

XX

KW Human parathyroid hormone; hPTH; PTH-related peptide; PTHrP; eczema;
 KW hyperproliferative skin disorder; psoriasis; ichthyosis; skin cancer;
 KW acne; actinic keratosis; alopecia; gene therapy.

XX

OS Homo sapiens.

XX

PN WO200228420-A2.

XX

PD 11-APR-2002.

XX

PF 05-OCT-2001; 2001WO-US31082.

XX

PR 06-OCT-2000; 2000US-238134P.

XX

PA (HOLI/) HOLICK M F.

XX

PI Holick MF;

XX
 DR WPI; 2002-452304/48.
 DR N-PSDB; AAD37995.
 XX
 PT Regulating mammalian skin or hair cell proliferation and
 PT differentiation by administering nucleic acids encoding peptides
 PT derived from N-terminal region of human parathyroid hormone (hPTH) or
 PT hPTH-related protein -
 XX
 PS Disclosure; Fig 8; 56pp; English.
 XX
 CC The invention relates to a method for regulating proliferation or
 CC enhancing differentiation of mammalian skin or hair cell. The method
 CC involves administering nucleic acids encoding peptides derived from
 CC N-terminal region of human parathyroid hormone (hPTH) or hPTH-related
 CC peptide (PTHrP). The method is used for inhibiting hyperproliferative
 CC skin disorders such as psoriasis, ichthyosis, eczema, acne, actinic
 CC keratosis, skin cancer, for inhibiting hair growth or preventing hair
 CC regrowth. It is useful for stimulating cell growth, rejuvenating aged
 CC skin, preventing skin wrinkles, treating skin wrinkles, enhancing wound
 CC healing, stimulating hair growth, maintaining hair growth, treating or
 CC preventing female or male pattern baldness, for treating chemotherapy
 CC induced alopecia and also for stimulating epidermal cell growth or
 CC hair follicle cell growth. The method is also used in gene therapy.
 CC The present sequence is hPTH peptide.
 XX
 SQ Sequence 31 AA;

Query Match 100.0%; Score 31; DB 23; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.1e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 7

AAU73039

ID AAU73039 standard; Peptide; 31 AA.

XX

AC AAU73039;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #21.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
 KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
 KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
 KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
 KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
 KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
 KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
 KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
 KW immunoglobulin G; IgG.

XX

OS Homo sapiens.
XX
PN WO200181415-A2.
XX
PD 01-NOV-2001.
XX
PF 27-APR-2001; 2001WO-US13528.
XX
PR 27-APR-2000; 2000US-200053P.
PR 28-JUN-2000; 2000US-214860P.
PR 06-FEB-2001; 2001US-266673P.
PR 26-APR-2001; 2001US-0843221.
XX
PA (AMGE-) AMGEN INC.
XX
PI Kostenuik P, Liu C, Lacey DL;
XX
DR WPI; 2002-066435/09.
XX
PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -
XX
PS Disclosure; Page 26; 107pp; English.
XX
CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid
CC arthritis, periodontal disease and alopecia. PTH receptor agonists are
CC useful as therapeutic agents in conditions including fracture repair
CC (including healing of non-union fractures), osteopenia, including various
CC forms of osteoporosis. AAU73018-AAU73181 represent parathyroid hormone
CC and parathyroid hormone related protein (PTH/PTHrP) modulators and
CC related amino acid sequences of the invention.
XX
SQ Sequence 31 AA;

Query Match 100.0%; Score 31; DB 23; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.1e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

AAU73176

ID AAU73176 standard; Peptide; 32 AA.

XX

AC AAU73176;

XX

DT 12-MAR-2002 (first entry)

XX

DE Parathyroid hormone PTH/PTHrP modulating domain #158.

XX

KW Human; parathyroid hormone; PTH; parathyroid hormone-related protein;
KW PTHrP; bone resorption inhibitor; osteoprotegrin; OPG; OPG-L antibody;
KW calcitonin; bisphosphonate; oestrogen; oestrogen receptor; tibolone;
KW osteopenia; hyperthyroidism; hypercalcaemia; tumour metastasis; bone;
KW breast cancer; prostate cancer; cachexia; anorexia; osteoporosis;
KW Paget's disease; osteomyelitis; osteonecrosis; bone cell death;
KW Gaucher's disease; sickle cell anaemia; systemic lupus erythematosus;
KW rheumatoid arthritis; periodontal disease; alopecia; fracture repair;
KW immunoglobulin G; IgG.

XX

OS Synthetic.

XX

PN WO200181415-A2.

XX

PD 01-NOV-2001.

XX

PF 27-APR-2001; 2001WO-US13528.

XX

PR 27-APR-2000; 2000US-200053P.

PR 28-JUN-2000; 2000US-214860P.

PR 06-FEB-2001; 2001US-266673P.

PR 26-APR-2001; 2001US-0843221.

XX

PA (AMGE-) AMGEN INC.

XX

PI Kostenuik P, Liu C, Lacey DL;

XX

DR WPI; 2002-066435/09.

XX

PT Composition, useful for treating osteopenia, comprises parathyroid
PT hormone and parathyroid hormone-related protein receptor modulators -

XX

PS Disclosure; Page 63; 107pp; English.

XX

CC The invention relates to a composition (I) comprising modulators of
CC parathyroid hormone (PTH) and parathyroid hormone-related protein (PTHrP)
CC which comprise a PTH/PTHrP modulating domain and a vehicle. (I)
CC comprising PTH agonist optionally with a bone resorption inhibitor, such
CC as osteoprotegrin (OPG), OPG-L antibody, calcitonin, bisphosphonates,
CC oestrogens, oestrogen receptor modulators and tibolone is useful for
CC treating osteopenia. (I) is useful for therapeutic and prophylactic
CC purposes. Antagonists of PTH receptor are useful in treating primary and
CC secondary hyperthyroidism, hypercalcaemia, tumour metastases,
CC particularly breast and prostate cancer, cachexia and anorexia,
CC osteopenia, including various forms of osteoporosis, Paget's disease of
CC bone, osteomyelitis, osteonecrosis or bone cell death, associated with
CC traumatic injury or nontraumatic necrosis associated with Gaucher's
CC disease, sickle cell anaemia, systemic lupus erythematosus, rheumatoid

PR 31-MAR-1981; 81JP-0048887.

XX

PA (TOXN) TOYO JOZO KK.

XX

DR WPI; 1983-709291/28.

XX

PT High activity human parathyroid hormone amide prodn. - by
PT condensing protected aminoacid(s) and/or peptide(s) useful for
PT lowering parathyroid gland function

XX

PS Claim 1; Page 1; 20pp; Japanese.

XX

CC The human parathyroid hormone, hPTH(1-34)-amide was prepd. by
CC the following steps: Firstly the carboxy gp. at the C-terminal
CC phenylalanine was converted into its amide form. The protected
CC individual amino acids were condensed, in order, by liquid phase
CC synthesis. The protecting groups were removed from the N-terminal
CC amino gp. and other functional gps. by acidolysis, and the
CC resulting hPTH(1-34)-amide purified by gel filtration
CC chromatography using a Sephadex G-25, G-50 or LH-20 column or by
CC column chromatography with carboxymethyl cellulose or ion exchange
CC resin. The peptide amide is useful in lowering the activity of the
CC parathyroid gland and in the prepn. of antibodies for diagnosis of
CC parathyroid gland function.

CC (Updated on 25-MAR-2003 to correct PR field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 4; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.5e-24;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

||||||||||||||||||||||||||||||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 11

AAP50377

ID AAP50377 standard; peptide; 34 AA.

XX

AC AAP50377;

XX

DT 25-MAR-2003 (updated)

DT 08-MAR-1992 (first entry)

XX

DE [Met(O)8,18]hPTH-(1-34).

XX

KW Human parathyroid hormone; calcium regulation.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 8

FT /label= oxidised methionine

FT Modified-site 18

FT /label= oxidised methionine

XX
 PN JP59204159-A.
 XX
 PD 19-NOV-1984.
 XX
 PF 28-APR-1983; 83JP-0075607.
 XX
 PR 28-APR-1983; 83JP-0075607.
 XX
 PA (TOXN) TOYO JOZO KK.
 XX
 DR WPI; 1985-003560/01.
 XX
 PT New (Met(O)8,18)hPTH-(1-34) peptide - increases calcium level in
 PT blood and decreases level in urine.
 XX
 PS Claim 1; Page 1; 3pp; Japanese.
 XX
 CC Unmodified hPTH(1-34) increases Ca in blood, decreases P in blood,
 CC decreases Ca in urine and increases P in urine by increasing cAMP in
 CC urine and enhancing vitamin D hydroxylase activity in kidneys. The
 CC modified derivative only has the effect of lowering Ca levels in
 CC urine and can be used when only this particular effect is required.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 CC (Updated on 25-MAR-2003 to correct DR field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 6; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 12

AAP60031

ID AAP60031 standard; peptide; 34 AA.

XX

AC AAP60031;

XX

DT 25-MAR-2003 (updated)

DT 06-JUL-1991 (first entry)

XX

DE Sequence of the first 34 AA residues of a parathyroid hormone
 DE obtainable from a human or animal.

XX

KW Osteoporosis therapy.

XX

OS Homo sapiens/animal.

XX

PN EP197514-A.

XX

PD 15-OCT-1986.

XX

PR 09-MAY-1988; 88US-0191512.
 XX
 PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Chorev M;
 XX
 DR WPI; 1990-354642/47.
 XX
 PT New para:thyroid hormone analogues - which inhibit hormone
 PT activity by binding receptors while not producing second
 PT messenger molecules
 XX
 PS Claim 1; Column 8; 6pp; English.
 XX
 CC Peptide analogues have high affinity for PTH cell surface receptors,
 CC but do not stimulate production of secondary messenger molecules.
 CC They may be used in inhibition of PTH action, and in diagnosis and
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
 CC Analogues may also be used in treatment of tumours and other cells
 CC overproducing peptide hormone-like substances, and immune diseases
 CC eg. allergic inflammation and hyperactive lymphocytes.
 CC Naturally occurring PTH levels may also be measured in vitro.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 14
 AAR07922

ID AAR07922 standard; protein; 34 AA.
 XX
 AC AAR07922;
 XX
 DT 18-FEB-1991 (first entry)
 XX
 DE Human parathyroid hormone analogue, Tyr34 hPTH(7-34).
 XX
 KW Osteoporosis; hypercalcemia; hyperparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 PN US4968669-A.
 XX
 PD 06-NOV-1990.
 XX
 PF 21-APR-1989; 89US-0341597.
 XX
 PR 21-APR-1989; 89US-0341597.
 PR 09-MAY-1988; 88US-0191512.
 XX

PA (MERI) MERCK & CO INC.
 XX
 PI Rosenblatt M, Chorev M;
 XX
 DR WPI; 1990-354642/47.
 XX
 PT New para:thyroid hormone analogues - which inhibit hormone
 PT activity by binding receptors while not producing second
 PT messenger molecules
 XX
 PS Claim 1; Column 8; 6pp; English.
 XX
 CC Peptide analogues have high affinity for PTH cell surface receptors,
 CC but do not stimulate production of secondary messenger molecules.
 CC They may be used in inhibition of PTH action, and in diagnosis and
 CC treatment of osteoporosis, hypercalcemia and hyperparathyroidism.
 CC Analogues may also be used in treatment of tumours and other cells
 CC overproducing peptide hormone-like substances, and immune diseases
 CC eg. allergic inflammation and hyperactive lymphocytes.
 CC Naturally occuring PTH levels may also be measured in vitro.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 15

AAR22283

ID AAR22283 standard; peptide; 34 AA.
 XX
 AC AAR22283;
 XX
 DT 29-JUL-1992 (first entry)
 XX
 DE Parathyroid hormone analogue N-terminus [1-34].
 XX
 KW Human; hPTH; wound healing; hair growth; hyperproliferation skin;
 KW disorders; psoriasis; cancer; burns.
 XX
 OS Homo sapiens.
 XX
 PN WO9204039-A.
 XX
 PD 19-MAR-1992.
 XX
 PF 30-AUG-1991; 91WO-US06218.
 XX
 PR 30-AUG-1990; 90US-0575219.
 XX
 PA (HOLI/) HOLICK M F.
 XX

PI Holick MF;
 XX
 DR WPI; 1992-114063/14.
 XX
 PT Use of peptide having homology with parathyroid hormone - for
 PT enhancement of cell proliferation for wound healing
 XX
 PS Disclosure; Fig 1; 34pp; English.
 XX
 CC The peptide can be easily synthesised by recombinant DNA or solid
 CC phase peptide synthesis techniques. The peptide has > 50 percent
 CC homology with the N-terminal 1-34 amino acids of human parathyroid
 CC hormone or hypercalcaemic region. It is esp. PTH (7-34). The
 CC peptide may be used in a method for the treatment of hyperprolifer-
 CC ation skin disorders e.g. psoriasis, cancers, burns or skin
 CC ulcerations by inhibition of cell proliferation and enhancement of
 CC cell differentiation (agonist activity). They are also used to
 CC enhance cell proliferation (antagonist activity) for wound healing.
 CC They are also applicable in the promotion of new hair growth or
 CC stimulation of the rate of hair growth e.g. following chemotherapy
 CC or for treating alopecia e.g. male pattern baldness.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 13; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 16

AAR41549

ID AAR41549 standard; protein; 34 AA.

XX

AC AAR41549;

XX

DT 25-MAR-2003 (updated)

DT 11-APR-1994 (first entry)

XX

DE [D-Ser3]hPTH (1-34)NH2.

XX

KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 3

FT /note = "D-form residue"

FT Modified-site 34

FT /note = "C terminal is amidated"

XX

PN EP561412-A1.

XX

PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.
 XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 17; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 17

AAR41570
 ID AAR41570 standard; protein; 34 AA.
 XX
 AC AAR41570;
 XX
 DT 25-MAR-2003 (updated)
 DT 11-APR-1994 (first entry)
 XX
 DE [Gln25]hPTH (1-34).
 XX
 KW PTH; parathyroid hormone; protease resistance; osteoporosis;
 KW hypoparathyroidism; hypertension.
 XX
 OS Homo sapiens.
 XX
 PN EP561412-A1.
 XX
 PD 22-SEP-1993.
 XX
 PF 18-MAR-1993; 93EP-0104500.

XX
 PR 19-MAR-1992; 92JP-0063517.
 PR 18-FEB-1993; 93JP-0029283.
 XX
 PA (TAKE) TAKEDA CHEM IND LTD.
 XX
 PI Fukuda T, Nakagawa S, Taketomi S;
 XX
 DR WPI; 1993-296712/38.
 XX
 PT New parathyroid hormone derivs. - used for the treatment of
 PT osteoporosis hypoparathyroidism and hypertension
 XX
 PS Example 1; Page 27; 37pp; English.
 XX
 CC Human parathyroid hormone (PTH) analogues (AAR41548 - generic sequence;
 CC AAR41549-R41582 - specific examples) show increased resistance to
 CC proteases and a greater persistency of activity within the blood is
 CC obtained. The proteins can be used to treat a number of bone and blood
 CC disorders. This analogue was used as a test compound.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 14; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 18

AAR58291

ID AAR58291 standard; peptide; 34 AA.

XX

AC AAR58291;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys(For)26, Lys(For)27]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 26

FT /label= Other

FT /note= "Formyl-Lys."

FT Modified-site 27

FT /label= Other

FT /note= "Formyl-Lys."

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 289; Page 47; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.5e-24;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 19

AAR58228

ID AAR58228 standard; peptide; 34 AA.

XX

AC AAR58228;

XX

DT 20-SEP-1994 (first entry)

XX
DE [D-Asp30]-hPTH(1-34)-NH2.
XX
KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 30
FT /note= "D-form residue."
FT Modified-site 34
FT /note= "in amide form"
XX
PN GB2269176-A.
XX
PD 02-FEB-1994.
XX
PF 12-JUL-1993; 93GB-0014384.
XX
PR 15-JUL-1992; 92GB-0015009.
PR 18-DEC-1992; 92GB-0026415.
PR 23-DEC-1992; 92GB-0026859.
PR 23-DEC-1992; 92GB-0026861.
PR 28-JAN-1993; 93GB-0001691.
PR 28-JAN-1993; 93GB-0001692.
PR 14-APR-1993; 93GB-0007673.
PR 19-APR-1993; 93GB-0008033.
XX
PA (SANO) SANDOZ LTD.
PA (BAUE/) BAUER W.
PA (SANO) SANDOZ PATENT GMBH.
PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
PI Waelchli R, Rainer A;
XX
DR WPI; 1994-018352/03.
XX
PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.
XX
PS Example 226; Page 45; 92pp; English.
XX
CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 20

AAR58232

ID AAR58232 standard; peptide; 34 AA.

XX

AC AAR58232;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Lys32]-hPTH(1-34)-NH2.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;
KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;
KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;

PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;

PI Waelchli R, Rainer A;

XX

DR WPI; 1994-018352/03.

XX

PT New active para-thyroid hormone variants - used for treating or
PT preventing osteoporosis etc.

XX

PS Example 230; Page 45; 92pp; English.

XX

CC This peptide is an example of a highly generic formula covering
CC parathyroid hormone variants useful for treating or preventing bone
CC conditions associated with calcium depletion/resorption, in cases
CC where calcium fixation is required (esp. osteoporosis) or to treat
CC hypoparathyroidism.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 21

AAR58181

ID AAR58181 standard; peptide; 34 AA.

XX

AC AAR58181;

XX

DT 20-SEP-1994 (first entry)

XX

DE [Thr33, Ala34]-hPTH(1-34)-NH₂.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

PR 18-DEC-1992; 92GB-0026415.

PR 23-DEC-1992; 92GB-0026859.

PR 23-DEC-1992; 92GB-0026861.

PR 28-JAN-1993; 93GB-0001691.

PR 28-JAN-1993; 93GB-0001692.

PR 14-APR-1993; 93GB-0007673.

PR 19-APR-1993; 93GB-0008033.

XX

PA (SANO) SANDOZ LTD.

PA (BAUE/) BAUER W.

PA (SANO) SANDOZ PATENT GMBH.

PA (SANO) SANDOZ-ERFINDUNGEN VERW GES MBH.

XX

PI Albert R, Bauer W, Breckenridge R, Cardinaux F;
 PI Gombert F, Gram H, Lewis I, Ramage P, Schneider H;
 PI Waelchli R, Rainer A;
 XX
 DR WPI; 1994-018352/03.
 XX
 PT New active para-thyroid hormone variants - used for treating or
 PT preventing osteoporosis etc.
 XX
 PS Example 179; Page 43; 92pp; English.
 XX
 CC This peptide is an example of a highly generic formula covering
 CC parathyroid hormone variants useful for treating or preventing bone
 CC conditions associated with calcium depletion/resorption, in cases
 CC where calcium fixation is required (esp. osteoporosis) or to treat
 CC hypoparathyroidism.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 15; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 22

AAR58016

ID AAR58016 standard; peptide; 34 AA.

XX

AC AAR58016;

XX

DT 20-SEP-1994 (first entry)

XX

DE N-alpha-Isopropyl-hPTH(1-34)-NH2 parathyroid hormone variant.

XX

KW Human parathyroid hormone; hPTH; variant; analogue;

KW calcium; depletion; fixation; resorption; osteopathy; osteoporosis;

KW hypoparathyroidism.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "N-alpha-isopropyl-Ser"

FT Modified-site 34

FT /note= "in amide form"

XX

PN GB2269176-A.

XX

PD 02-FEB-1994.

XX

PF 12-JUL-1993; 93GB-0014384.

XX

PR 15-JUL-1992; 92GB-0015009.

XX

XX

XX

XX

XX

XX

XX

1

Query Match 100.0%; Score 31; DB 15; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLODV 31

RESULT 23

AAR58017

XX

XX

XX

XX

XX

XX


```

FH   Key                               Location/Qualifiers
FT   Modified-site                     26
FT                                     /note= "N-epsilon-Isopropyl-Lys"
FT   Modified-site                     27
FT                                     /note= "N-epsilon-Isopropyl-Lys"
FT   Modified-site                     34
FT                                     /note= "in amide form"
XX
PN   GB2269176-A.
XX
PD   02-FEB-1994.
XX
PF   12-JUL-1993;   93GB-0014384.
XX
PR   15-JUL-1992;   92GB-0015009.
PR   18-DEC-1992;   92GB-0026415.
PR   23-DEC-1992;   92GB-0026859.
PR   23-DEC-1992;   92GB-0026861.
PR   28-JAN-1993;   93GB-0001691.
PR   28-JAN-1993;   93GB-0001692.
PR   14-APR-1993;   93GB-0007673.
PR   19-APR-1993;   93GB-0008033.
XX
PA   (SANO ) SANDOZ LTD.
PA   (BAUE/) BAUER W.
PA   (SANO ) SANDOZ PATENT GMBH.
PA   (SANO ) SANDOZ-ERFINDUNGEN VERW GES MBH.
XX
PI   Albert R,  Bauer W,  Breckenridge R,  Cardinaux F;
PI   Gombert F,  Gram H,  Lewis I,  Ramage P,  Schneider H;
PI   Waelchli R,  Rainer A;
XX
DR   WPI; 1994-018352/03.
XX
PT   New active para-thyroid hormone variants - used for treating or
PT   preventing osteoporosis etc.
XX
PS   Example 2; Page 32; 92pp; English.
XX
CC   This peptide is an example of a highly generic formula covering
CC   parathyroid hormone variants useful for treating or preventing bone
CC   conditions associated with calcium depletion/resorption, in cases
CC   where calcium fixation is required (esp. osteoporosis) or to treat
CC   hypoparathyroidism.
XX
SQ   Sequence    34 AA;

Query Match          100.0%;  Score 31;  DB 15;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 4.5e-24;
Matches    31;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy          1  SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
           ||||||||||||||||||||||||||||
Db          1  SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 24

AAR55724

ID AAR55724 standard; peptide; 34 AA.

XX

AC AAR55724;

XX

DT 25-MAR-2003 (updated)

DT 16-NOV-1994 (first entry)

XX

DE Parathormone N-terminal sequence.

XX

KW Parathormone; parathyroid hormone; fatty acyl-peptide; conjugate;

KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; DHA;

KW eicosapentaenoic acid; EPA; antitumor.

XX

OS Synthetic.

XX

PN WO9412530-A1.

XX

PD 09-JUN-1994.

XX

PF 29-NOV-1993; 93WO-HU00065.

XX

PR 30-NOV-1992; 92US-0984293.

XX

PA (BIOS-) BIOSIGNAL KUTATO FEJLESZTO KFT.

PA (SYNT-) SYNTHETIC PEPTIDES INC.

XX

PI Balogh A, Cachia PJ, Hodges RS, Horvath A, Keri G;

PI Szederkenyi F, Vadasz Z;

XX

DR WPI; 1994-200194/24.

XX

PT New fatty acyl-peptide conjugates for inhibiting cell

PT proliferation - more active than free peptide, partic. for

PT treating tumours, virus-infected cells, psoriasis, etc.

XX

PS Disclosure; Fig. 1; 45pp; English.

XX

CC The peptides given in AAR55718-48 can each be conjugated through an

CC amide linkage with a polyunsaturated fatty acid moiety, such as

CC docosahexaenoic acid (DHA) or eicosapentanoic acid, to improve

CC antiproliferative activity. The parathormone N-terminal fragment

CC inhibits osteoblast proliferation.

CC (Updated on 25-MAR-2003 to correct PN field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 15; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.5e-24;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 25

AAR74521
 ID AAR74521 standard; Peptide; 34 AA.
 XX
 AC AAR74521;
 XX
 DT 25-MAR-2003 (updated)
 DT 04-DEC-1995 (first entry)
 XX
 DE Human parathyroid hormone (1-34).
 XX
 KW Analogue; truncated human parathyroid hormone; PTH; hPTH; substitution;
 KW osteoporosis; hypercalcaemia; hyperparathroidism;
 KW metabolic bone disease; human; veterinary medicine;
 KW iontophoretic transdermal transport; recombinant E.coli.
 XX
 OS Homo sapiens.
 XX
 PN WO9511988-A1.
 XX
 PD 04-MAY-1995.
 XX
 PF 25-OCT-1994; 94WO-US12205.
 XX
 PR 25-OCT-1993; 93US-0142551.
 XX
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Oldenburg KR, Selick HE;
 XX
 DR WPI; 1995-178880/23.
 XX
 PT New active analogues of parathyroid hormone - with increased
 PT activity, stability in serum etc., esp. for treating
 PT osteoporosis, also related DNA and vectors
 XX
 PS Disclosure; Page 1; 109pp; English.
 XX
 CC This sequence represents residues 1-34 of human parathyroid hormone
 CC (RPTH). This sequence was used in the production of analogues of the
 CC truncated form of PTH. These analogues have increased activity and
 CC longer serum half life than native PTH due to eg. substitution of Met
 CC residues with Leu residues and replacing the carboxy Phe with Tyr. The
 CC carboxy terminal may also be modified by the addition of a homoserine
 CC residue or analogue, or by the addition of residues 35-84 of wild type
 CC PTH (see AAR74410). These PTH analogues may be used in the treatment of
 CC osteoporosis or hypercalcaemia, hyperparathroidism or other metabolic
 CC bone diseases in human or veterinary medicine. These peptides may also
 CC have increased iontophoretic transdermal transport compared to wild type
 CC PTH and can be produced in high yield in recombinant E.coli.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 16; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 26

AAW99449

ID AAW99449 standard; peptide; 34 AA.

XX

AC AAW99449;

XX

DT 08-JUN-1999 (first entry)

XX

DE Human parathyroid hormone aal-34.

XX

KW Parathyroid hormone; PTH; parathormone; premature birth; pregnancy;
 KW spontaneous abortion; uterine contraction; human.

XX

OS Homo sapiens.

XX

PN US5880093-A.

XX

PD 09-MAR-1999.

XX

PF 05-APR-1995; 95US-0411726.

XX

PR 28-SEP-1992; 92IT-MI02331.

XX

PA (BAGN/) BAGNOLI F.

XX

PI Bagnoli F;

XX

DR WPI; 1996-162392/17.

XX

PT Use of composition containing parathormone or fragments - for
 PT preventing premature birth or spontaneous abortion or for treating
 PT unwanted uterine contractions

XX

PS Disclosure; Column 7-8; 11pp; English.

XX

CC Peptides AAW99448-W99452 represent all or part of the parathyroid
 CC hormone (PTH; parathormone) sequence or related peptide. The peptides
 CC are used for preventing premature birth, spontaneous abortion or unwanted
 CC uterine contractions in a pregnant human patient.
 CC (Note: this patent is the first Major Country Equivalent to Italian
 CC Patent IT1255388).

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 17; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 27

AAR99978

ID AAR99978 standard; peptide; 34 AA.

XX

AC AAR99978;

XX

DT 30-APR-1997 (first entry)

XX

DE Human parathyroid hormone peptide fragment (1-34).

XX

KW cyclic parathyroid hormone fragment; calcium-regulating activity;
KW osteoporosis; inhibit proliferation; epidermal cell; psoriasis;
KW improved half life; calcium retention; bone.

XX

OS Synthetic.

XX

PN DE19508672-A1.

XX

PD 12-SEP-1996.

XX

PF 10-MAR-1995; 95DE-1008672.

XX

PR 10-MAR-1995; 95DE-1008672.

XX

PA (BOEF) BOEHRINGER MANNHEIM GMBH.

XX

PI Dony C, Esswein A, Hoffmann E, Honold K, Schaefer W;

XX

DR WPI; 1996-413519/42.

XX

PT Cyclic parathyroid hormone fragments with lactam bridge - have good
PT in vivo half life and are useful for treating osteoporosis and
PT preventing epidermal cell proliferation

XX

PS Disclosure; Page 9; 14pp; German.

XX

CC New cyclic parathyroid hormone fragments (CPTH) have the amino acid
CC sequence of h, b, p, r or cPTH(1-34), opt. extended by up to 4 amino
CC acids (aa) at the C-terminus and opt. shortened by up to 3 amino acids at
CC the N-terminus, and are cyclised between positions 13 and 17. One of
CC these positions is occupied by L- or D- Orn or Lys, and the other by L-
CC or D- Glu or Asp. CPTH have calcium-regulating activity (esp. for
CC treating osteoporosis and inhibit proliferation of epidermal cells (for
CC treating psoriasis). The CPTH have an improved half life in vivo than
CC known PTH fragments, increased mitogenicity and DNA-synthesising
CC capacity, reduced catabolic, calcium-mobilising activity and increased
CC activity for calcium retention and incorporation into bone. The
CC present sequence is that of human PTH peptide fragment (1-34).

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.5e-24;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 28

AAR98951

ID AAR98951 standard; peptide; 34 AA.

XX

AC AAR98951;

XX

DT 15-JAN-1997 (first entry)

XX

DE Target peptide (PTH(1-34)) used in fusion protein construct.

XX

KW Fusion protein construct; isolation; purification;

KW growth hormone releasing factor; glucagon-like peptide 1;

KW parathyroid hormone; inclusion body; carbonic anhydrase.

XX

OS Synthetic.

XX

PN WO9617942-A1.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15800.

XX

PR 07-DEC-1994; 94US-0350530.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI De LA MOTTE RS, Henriksen DB, Holmquist B, Manning SD;

PI Partridge BE, Stout JS, Wagner FW;

XX

DR WPI; 1996-287186/29.

XX

PT Isolation and purificn of peptide(s) from fusion protein constructs

PT - which include a carbonic anhydrase and a variable fused

PT polypeptide

XX

PS Claim 18; Page 48; 67pp; English.

XX

CC A new method for the isolation and/or purification of a recombinant
CC peptide employs a fusion protein construct (FPC) comprising a
CC carbonic anhydrase and a variable fused polypeptide containing a
CC target peptide. The method comprises precipitating either the FPC or
CC a fragment of the FPC including the carbonic anhydrase. An
CC alternative method of producing the peptide comprises expressing the
CC FPC as part of an inclusion body. The target peptides of the FPC are
CC derived from growth hormone releasing factor (GRF), glucagon-like
CC peptide 1 (GLP1) or parathyroid hormone (PTH). This sequence
CC corresponds to amino acids 1-34 of PTH.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.5e-24;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 29

AAR98966

ID AAR98966 standard; Peptide; 34 AA.

XX

AC AAR98966;

XX

DT 02-DEC-1996 (first entry)

XX

DE PTH(1-34).

XX

KW PTH; parathyroid hormone; parathormone; C-amide;

KW C-amidated peptide; alpha-carboxamide; recombinant protein;

KW fusion protein; transpeptidation.

XX

OS Not specified.

XX

PN WO9617941-A2.

XX

PD 13-JUN-1996.

XX

PF 07-DEC-1995; 95WO-US15799.

XX

PR 07-DEC-1994; 94US-0350528.

XX

PA (BION-) BIONEBRASKA INC.

XX

PI Heriksen DB, Holmquist B, Patridge BE, Stout JS;

PI Wagner FW;

XX

DR WPI; 1996-287185/29.

XX

PT Production of C-terminal alpha-carboxamidated peptide(s) - by
 PT cleavage and transpeptidation of recombinant multicopy peptide(s) or
 PT fusion constructs

XX

PS Claim 12; Page 70; 93pp; English.

XX

CC GLP1(7-35), GRF(1-44) and PTH(1-34) peptides (AAR98964-66) can be
 CC produced as C-terminal amidated peptides utilising novel recombinant
 CC protein constructs (see also AAR98967-72) in which single or multiple
 CC copies of the peptide are linked by intraconnecting peptides that
 CC permit the construct to be selectively reacted to produce product
 CC peptides having a C-terminal alpha-carboxamide. Expression cassettes
 CC (see also AAT34865-70) can be incorporated into vectors allowing prodn.
 CC of the recombinant proteins in transformed E. coli host cells.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 17; Length 34;

Best Local Similarity 100.0%; Pred. No. 4.5e-24;

Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 30

AAR88835

ID AAR88835 standard; peptide; 34 AA.

XX

AC AAR88835;

XX

DT 07-OCT-1996 (first entry)

XX

DE Human parathyroid hormone analogue, cyclo-PTH(1-34)-NH2.

XX

KW Parathyroid hormone; PTH; analogue; osteoporosis; bone cell;

KW calcium regulation; reduced PKC activity; protein kinase C;

KW increased adenylyl cyclase activity; cAMPase; cyclic; bone loss.

XX

OS Synthetic.

XX

FH	Key	Location/Qualifiers
----	-----	---------------------

FT	Modified-site	10
----	---------------	----

FT		/note= "forms peptide bond with Lys at posn. 26"
----	--	--

FT	Modified-site	14
----	---------------	----

FT		/note= "forms peptide bond with Asp at posn. 30"
----	--	--

FT	Modified-site	26
----	---------------	----

FT		/note= "forms peptide bond with Asn at posn. 10"
----	--	--

FT	Modified-site	30
----	---------------	----

FT		/note= "forms peptide bond with His at posn. 14"
----	--	--

FT	Modified-site	34
----	---------------	----

FT		/note= "amidated"
----	--	-------------------

XX

PN CA2126299-A.

XX

PD 21-DEC-1995.

XX

PF 20-JUN-1994; 94CA-2126299.

XX

PR 20-JUN-1994; 94CA-2126299.

XX

PA (WILL/). WILICK G E.

XX

PI Neugebauer W, Sung WL, Surewicz W, Whitfield JF;

PI Willick GE;

XX

DR WPI; 1996-151754/16.

XX

PT New human parathyroid hormone analogues - which have increased

PT adenylyl cyclase activating activity, used for treating osteoporosis

XX

PS Claim 3; Fig 8; 21pp; English.

XX

CC AAR88829-R88841 are human parathyroid hormone (hPTH) analogues. The

CC analogues increase G-protein coupled adenylyl cyclase (cAMPase)

CC activity and reduce protein kinase C (PKC) activity. The analogues

CC can reverse the loss of bone and increase bone mass and density
CC without undesirable effects. They are useful for the treatment of
CC osteoporosis and other bone related disorders and disorders
CC involving bone cell calcium regulation.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 31

AAW24273

ID AAW24273 standard; protein; 34 AA.

XX

AC AAW24273;

XX

DT 17-OCT-1997 (first entry)

XX

DE Wild type parathyroid hormone.

XX

KW Analogue; parathyroid hormone; PTH; hirudin; hirulog;
KW electrotransportability; alpha-helix; beta-sheet.

XX

OS Homo sapiens.

XX

PN WO9639423-A2.

XX

PD 12-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09647.

XX

PR 06-JUN-1995; 95US-0468275.

XX

PA (ALZA) ALZA CORP.

XX

PI Holladay LA, Oldenburg KR;

XX

DR WPI; 1997-043058/04.

XX

PT Prepn. of analogues of parent poly-peptide(s), esp. parathyroid
PT hormone and hirulog - which exhibit better or enhanced
PT electro-transportability through a body surface

XX

PS Claim 7; Fig 1A; 55pp; English.

XX

CC The sequences given in AAW24273-76 represent wildtype and analogues of
CC parathyroid hormone (PTH). The analogues exhibit better/enhanced
CC electrotransportability through a body surface, and are characterised
CC by substituting one or more amino acid residues of the parent
CC polypeptide to disrupt one or more alpha-helical and/or beta-sheet
CC segments of the parent polypeptide. An electrotransport device can

CC deliver the polypeptide analogue through a body surface by electro-
CC transport by including providing a therapeutically effective amount
CC of the polypeptide analogue in a donor reservoir of the electrotransport
CC device. The electrotransport flux of a polypeptide is increased by
CC reducing the potential of the polypeptide for forming alpha-helix or
CC beta-sheet segment.

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 32

AAW19994

ID AAW19994 standard; peptide; 34 AA.

XX

AC AAW19994;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;
KW adenylate cyclase activity; bone growth; osteoporosis; fracture;
KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 13

FT /note= "joined via amide bond to residue 17"

FT Misc-difference 17

FT /note= "joined via amide bond to residue 13"

FT Misc-difference 34

FT /note= "amidated"

XX

PN WO9640193-A1.

XX

PD 19-DEC-1996.

XX

PF 06-JUN-1996; 96WO-US09674.

XX

PR 07-JUN-1995; 95US-0488105.

XX

PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.

XX

PI Chorev M, Rosenblatt M;

XX

DR WPI; 1997-051884/05.

XX

PT New cyclic analogues of parathyroid hormone - having di:sulphide or

XX
PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
XX
PI Chorev M, Rosenblatt M;
XX
DR WPI; 1997-051884/05.
XX
PT New cyclic analogues of parathyroid hormone - having di:sulphide or
PT amide bond between residues 13 and 17 and/or between residues 26 and
PT 30, useful for treating osteoporosis and bone fractures
XX
PS Claim 6; Page -; 23pp; English.
XX
CC AAW20000 is a cyclised peptide derived from the N-terminal sequence
CC of human parathyroid hormone (PTH). The peptide is able to bind to
CC PTH receptors and stimulate adenylate cyclase activity. Cyclised
CC PTH peptides stimulate bone growth and thus are useful in the
CC treatment of osteoporosis and bone fractures. Optionally they may
CC be administered concurrently with antiresorptive therapy (e.g.
CC bisphosphonate and calcitonin).
CC N.B. sequence not given in the specification, created from known
CC sequence of amino acids 1-34 of human PTH.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 18; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 34

AAW20006

ID AAW20006 standard; peptide; 34 AA.

XX

AC AAW20006;

XX

DT 28-AUG-1997 (first entry)

XX

DE Cyclised human parathyroid hormone (1-34) amide.

XX

KW Parathyroid hormone; PTH; amino terminus; cyclic; analogue;
KW adenylate cyclase activity; bone growth; osteoporosis; fracture;
KW antiresorptive therapy.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Misc-difference 13

FT /note= "joined via amide bond to residue 17"

FT Misc-difference 17

FT /note= "joined via amide bond to residue 13"

FT Misc-difference 26

FT /note= "joined via amide bond to residue 30"

FT Misc-difference 30
 FT /note= "joined via amide bond to residue 26"
 FT Misc-difference 34
 FT /note= "amidated"
 XX
 PN WO9640193-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US09674.
 XX
 PR 07-JUN-1995; 95US-0488105.
 XX
 PA (BETH-) BETH ISRAEL HOSPITAL ASSOC.
 XX
 PI Chorev M, Rosenblatt M;
 XX
 DR WPI; 1997-051884/05.
 XX
 PT New cyclic analogues of parathyroid hormone - having di:sulphide or
 PT amide bond between residues 13 and 17 and/or between residues 26 and
 PT 30, useful for treating osteoporosis and bone fractures
 XX
 PS Claim 8; Page -; 23pp; English.
 XX
 CC AAW20006 is a cyclised peptide derived from the N-terminal sequence
 CC of human parathyroid hormone (PTH). The peptide is able to bind to
 CC PTH receptors and stimulate adenylate cyclase activity. Cyclised
 CC PTH peptides stimulate bone growth and thus are useful in the
 CC treatment of osteoporosis and bone fractures. Optionally they may
 CC be administered concurrently with antiresorptive therapy (e.g.
 CC bisphosphonate and calcitonin).
 CC N.B. sequence not given in the specification, created from known
 CC sequence of amino acids 1-34 of human PTH.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 35

AAW17955

ID AAW17955 standard; peptide; 34 AA.

XX

AC AAW17955;

XX

DT 29-JUL-1997 (first entry)

XX

DE Human parathyroid hormone analogue [Aib34]hPTH(1-34)NH2.

XX

KW Osteoporosis; agonist; PTH; human; anti-resorptive therapy;

KW bone fracture.
 XX
 OS Homo sapiens.
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 34
 FT /label= Aib
 FT /note= "In amide form"
 XX
 PN WO9702834-A1.
 XX
 PD 30-JAN-1997.
 XX
 PF 03-JUL-1996; 96WO-US11292.
 XX
 PR 29-MAR-1996; 96US-0626186.
 PR 13-JUL-1995; 95US-0001105.
 PR 06-SEP-1995; 95US-0003305.
 XX
 PA (BIOM-) BIOMEASURE INC.
 XX
 PI Dong ZX;
 XX
 DR WPI; 1997-118819/11.
 XX
 PT New variants of human parathyroid hormone 1-34 peptide - which
 PT stimulate bone growth and are used for treatment of osteoporosis and
 PT bone fracture
 XX
 PS Claim 11; Page -; 33pp; English.
 XX
 CC The present sequence is a specific example of a human parathyroid
 CC hormone (hPTH) analogue from fragment 1-34 in which at least one
 CC of the amino acid residues at positions 3, 12, 16, 17, 19 and 34
 CC is alpha-aminoisobutyric acid (Aib). In this example the Phe residue
 CC at position 34 of the wild-type has been substituted by Aib. The hPTH
 CC analogues stimulate bone growth and so are useful in human or veterinary
 CC medicine for treatment of osteoporosis and bone fracture, optionally in
 CC conjunction with anti-resorptive therapy (bisphosphonates and
 CC calcitonin).
 CC N.B. The present sequence does not appear in the specification. It
 CC corresponds to the known hPTH 1-34 fragment with the modifications
 CC as stated in the claim.
 XX
 SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 18; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.5e-24;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

AAW67291

ID AAW67291 standard; peptide; 34 AA.

XX

AC AAW67291;

XX

DT 22-DEC-1998 (first entry)

XX

DE Parathyroid hormone analogue #18.

XX

KW Parathyroid hormone; parathormone; bone growth; bone fracture;
KW osteoporosis; anti-resorptive therapy; calcitonin.

XX

OS Synthetic.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Modified-site 12

FT /note= "1-amino-1-cyclohexanecarboxylic acid"

FT Modified-site 34

FT /note= "C-terminal amide"

XX

PN W09830590-A2.

XX

PD 16-JUL-1998.

XX

PF 08-DEC-1997; 97WO-US22498.

XX

PR 07-MAR-1997; 97US-0813534.

PR 07-JAN-1997; 97US-0779768.

XX

PA (BIOM-) BIOMEASURE INC.

XX

PI Dong ZX;

XX

DR WPI; 1998-399065/34.

XX

PT Parathyroid hormone analogue peptide compounds - used for
PT stimulating bone growth, e.g. in treatment of bone fractures or
PT osteoporosis

XX

PS Claim 6; Page -; 24pp; English.

XX

CC The invention relates to peptides of formula (I) containing at least one
CC Acc (i.e. 1-amino-1-(3-9C cycloalkane)-carboxylic acid) residue.
CC (R1) (R2) A1-Val-A3-Glu-A5-Gln-A7-A8-His-Asn-A11-A12-Lys-His-A15-A-16-A17-
CC A-18-A19-Arg-A21-A22-A23-A24-Arg-Lys-A27-A28-A29-A30-A31-A32-A33-A34-R3
CC (I); where A1 = Ser, Ala or Dap; A3, A17 = Ser, Thr or Aib; A5, A7, A11,
CC A15 = Leu, Nle, Ile, Cha, beta -Nal, Trp, Pal, Acc, Phe or p-(X)-Phe; X
CC = OH, halo or Me; A8 = Met, Nva, Leu, Val, Ile, Cha, Acc or Nle; A12 =
CC Gly, Acc or Aib; A16 = Ser, Asn, Ala or Aib; A18 = Met, Nva, Leu, Val,
CC Ile, Nle, Acc, Cha or Aib; A19 = Glu or Aib; A21 = Val, Acc, Cha or Met;
CC A22 = Acc or Glu; A'23 = Trp, Acc or Cha; A24, A28 = Leu, Acc or Cha; A27
CC = Lys, Aib, Leu, hArg, Gln, Acc or Cha; A29 = Glu, Acc or Aib; A30 = Asp
CC or Lys; A31 = Val, Leu, Nle, Acc or Cha, or is deleted; A32 = His or is
CC deleted; A33 = Asn or is deleted; A34 = Phe, Tyr, Amp or Aib, or is
CC deleted; R1,R2 = H, 1-12C alkyl, 2-12C alkenyl, 7-20C phenylalkyl,
CC 11-20C naphthylalkyl, 1-12C hydroxyalkyl, 2-12C hydroxyalkenyl, 7-20C

PT Recombinant production of modified parathyroid hormone or related
PT peptide - having bone mass restoring activity which differs from
PT naturally occurring PTH or PTHrP by changes comprising substitutions
PT at one or more of positions 22-31

XX

PS Disclosure; Column 1/2; 65pp; English.

XX

CC The parathyroid hormone (PTH) analogues AAW61658-W61732 differ from
CC naturally occurring PTH by changes comprising substitutions at on or
CC more of positions 22-31. The bone mass restoring activity of the PTH
CC analogues can be used to treat or prevent conditions characterised by
CC a decrease in bone mass, e.g. osteoporosis or osteopenia.
CC (Updated on 25-MAR-2003 to correct PF field.)

XX

SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 19; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 38

AAW65975

ID AAW65975 standard; peptide; 34 AA.

XX

AC AAW65975;

XX

DT 25-MAR-2003 (updated)

DT 13-NOV-1998 (first entry)

XX

DE Human parathyroid hormone N-terminal fragment (residues 1-34).

XX

KW Parathyroid hormone; PTH; parathyroid hormone related peptide; PTHrp;
KW bone mass; trabecular bone; bone resorption; osteoporosis.

XX

OS Homo sapiens.

XX

PN US5807823-A.

XX

PD 15-SEP-1998.

XX

PF 24-MAY-1995; 95US-0449317.

XX

PR 18-JAN-1994; 94US-0184328.

PR 14-JUL-1992; 92US-0915247.

PR 24-MAY-1995; 95US-0449317.

XX

PA (SYNT) SYNTEX USA INC.

XX

PI Krstenansky JL, Nestor JJ, Vickery BH;

XX

DR WPI; 1998-520168/44.

XX

PT Treatment of osteoporosis - by administration of modified
PT parathyroid hormone peptides
XX
PS Disclosure; Columns 1-2; 71pp; English.
XX
CC The invention relates to treatment of mammalian conditions characterised
CC by decreases in bone mass. The treatment comprises administering a
CC modified parathyroid hormone (PTH) or parathyroid hormone related peptide
CC (PTHrp) that differs from naturally occurring PTH or PTHrp by one or more
CC amino acid substitutions in positions 22-31. PTH and PTHrp are useful for
CC treatment of disorders characterised by decreasing bone mass, especially
CC osteoporosis. Use of PTH or PTHrp gives a sustainable increase in
CC trabecular bone by a different method to the prior art, which slowed down
CC bone resorption. The present sequence represents the N-terminal fragment
CC of human PTH (residues 1-34).
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 19; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 39

AAW42614

ID AAW42614 standard; peptide; 34 AA.

XX

AC AAW42614;

XX

DT 24-JUN-1998 (first entry)

XX

DE Human parathyroid hormone N-terminal fragment.

XX

KW Parathyroid hormone; PTH; osteoporosis; peptide synthesis; analogue;
KW parathyroid hormone-related hormone; PTH-rP; alpha-helix; amphipathic.

XX

OS Homo sapiens.

XX

PN EP822200-A1.

XX

PD 04-FEB-1998.

XX

PF 23-JUL-1997; 97EP-0112595.

XX

PR 30-JUL-1996; 96US-0023322.

XX

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX

PI Arzeno HB;

XX

DR WPI; 1998-102869/10.

XX

PT Chemical synthesis of parathyroid hormone analogues - by solution or
PT solid-phase methods, useful for treating osteoporosis
XX
PS Disclosure; Page 3; 69pp; English.
XX
CC This sequence is shown in the specification. The invention relates to
CC a process for synthesising a polypeptide analogue of parathyroid hormone
CC (PTH) or PTH-related peptide (PTH-rP) in which amino acids 22-31 are:
CC Glu-Leu-Leu-Glu-Lys-Leu-Leu-Xaa1-Lys-Leu (I); Glu-Leu-Leu-Glu-Arg-Leu-
CC Leu-Xaa2-Arg-Leu (II); Ala-Leu-Ala-Glu-Ala-Leu-Ala-Glu-Ala-Leu (III);
CC Ser-Leu-Leu-Ser-Ser-Leu-Leu-Ser-Ser-Leu (IV); Ala-Phe-Tyr-Asp-Lys-Val-
CC Ala-Glu-Lys-Leu (V); Xaa3-Xaa4-Leu-Xaa3-Xaa5-Leu-Xaa6-Xaa7-Xaa8-Xaa6
CC (VI); or Xaa3-Xaa4-Leu-Xaa3-Arg-Leu-Leu-Xaa9-Arg-Leu (VII), Xaa1 = Glu
CC or Arg; Xaa2 = Glu, Lys or 'lysine-(OCCH2PEGX)'; Xaa3 = Glu, Glu(OMe),
CC His or Phe; Xaa4 = Leu or Phe; Xaa5 = Lys or His; Xaa6 = Leu or Ile;
CC Xaa7 = Ala, Arg or Glu; Xaa8 = Lys or Glu; and Xaa9 = Glu, Lys or '
CC Lys(COCH2PEGX)'. The process comprises independently synthesising
CC precursor peptide fragments of the polypeptide by solution or solid-
CC phase techniques, coupling (condensing) the fragments together, and
CC removing any protecting groups. The peptides can be used for treating
CC osteoporosis.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 19; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 40

AAW48392

ID AAW48392 standard; peptide; 34 AA.

XX

AC AAW48392;

XX

DT 07-JUL-1998 (first entry)

XX

DE Human parathyroid hormone biologically active region.

XX

KW Parathyroid hormone related protein; PTH-2 receptor; PTHrP;
KW osteoporosis; calcium homeostasis.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT Region 5

FT /note= "Determines signalling capability"

FT Region 23

FT /note= "Determines binding affinity"

XX

PN WO9804591-A1.

XX

PD 05-FEB-1998.

XX
PF 30-JUL-1997; 97WO-US13360.
XX
PR 31-JUL-1996; 96US-0025471.
XX
PA (GARD/) GARDELLA T J.
PA (JUEP/) JUEPPNER H.
XX
PI Gardella TJ, Jueppner H;
XX
DR WPI; 1998-130622/12.
XX
PT Parathyroid hormone-related peptide analogues with agonist activity
PT - at PTH/PTHrP receptor and either agonist or antagonist activity at
PT PTH-2 receptor, used e.g. for treatment of osteoporosis
XX
PS Disclosure; Fig 3; 48pp; English.
XX
CC The present sequence represents the biologically active region of
CC human parathyroid hormone (PTH). PTH is a major regulator of
CC calcium homeostasis whose principal target cells occur in bone and
CC kidney. Some of the renal and skeletal actions of PTH appear to be
CC mimicked by PTH related protein (PTHrP) which are believed to interact
CC with the PTH receptor in these tissues. The invention creates hybrids
CC (AAW48394-W48398) of the active regions of PTH and PTHrP (AAW48393) to
CC determine the residues involved in ligand-specificity of the PTH-2
CC receptor. It was found that ILE 5 determined signalling capabilities
CC while TRP 23 determined binding affinity. The invention shows that by
CC changing these two residues in PTHrP to the corresponding residues
CC in PTH, PTHrP peptide analogues are created which are claimed to be
CC selective agonists or antagonists of the PTH-2 receptor (AAW48399 and
CC AAW48400). The antagonistic PTHrP peptide analogues are claimed to be
CC useful in treating diseases involving altered or excessive activation of
CC PTH-2 receptors (by inhibiting activation) while agonistic PTHrP
CC peptide analogues are claimed to be useful in treating osteoporosis (by
CC activating both PTH and PTH-2 receptors). PTHrP analogues are also
CC useful for studying biological roles of the PTH-2 receptor and to
CC identify specific sites of ligand-receptor interaction.
XX
SQ Sequence 34 AA;

Query Match 100.0%; Score 31; DB 19; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.5e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Search completed: January 14, 2004, 10:34:24
Job time : 31.648 secs

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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:59 ; Search time 10.5265 Seconds
(without alignments)
124.604 Million cell updates/sec

Title: US-09-843-221A-165
Perfect score: 31
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 25778

Minimum DB seq length: 28

Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	31	100.0	31	2	US-08-691-647C-1	Sequence 1, Appli
3	31	100.0	31	2	US-08-691-647C-6	Sequence 6, Appli
4	31	100.0	31	3	US-08-904-760B-1	Sequence 1, Appli
5	31	100.0	31	3	US-08-904-760B-6	Sequence 6, Appli
6	31	100.0	31	3	US-08-904-760B-14	Sequence 14, Appl
7	31	100.0	31	3	US-08-904-760B-32	Sequence 32, Appl
8	31	100.0	31	4	US-09-406-813-2	Sequence 2, Appli
9	31	100.0	31	4	US-09-536-785A-1	Sequence 1, Appli
10	31	100.0	31	4	US-09-536-785A-6	Sequence 6, Appli
11	31	100.0	31	4	US-09-536-785A-14	Sequence 14, Appl

12	31	100.0	31	4	US-09-536-785A-32	Sequence 32, Appl
13	31	100.0	33	4	US-09-447-800-9	Sequence 9, Appli
14	31	100.0	34	1	US-07-765-373-1	Sequence 1, Appli
15	31	100.0	34	1	US-08-033-099-1	Sequence 1, Appli
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39	31	100.0	34	4	US-09-635-076-1	Sequence 1, Appli
40	31	100.0	34	4	US-09-228-990-1	Sequence 1, Appli
41	31	100.0	34	4	US-09-447-800-8	Sequence 8, Appli
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170	13	41.9	34	1	US-08-488-105-6	Sequence 6, Appli
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172	13	41.9	34	1	US-08-488-105-11	Sequence 11, Appl
173	13	41.9	34	1	US-08-488-105-16	Sequence 16, Appl
174	13	41.9	34	1	US-08-488-105-18	Sequence 18, Appl
175	13	41.9	34	1	US-08-449-500-79	Sequence 79, Appl
176	13	41.9	34	1	US-08-449-317A-79	Sequence 79, Appl
177	13	41.9	34	2	US-08-142-551B-3	Sequence 3, Appli
178	13	41.9	34	2	US-08-477-022-79	Sequence 79, Appl
179	13	41.9	34	2	US-08-449-447-79	Sequence 79, Appl
180	13	41.9	34	2	US-08-184-328-79	Sequence 79, Appl
181	13	41.9	34	2	US-08-521-097-79	Sequence 79, Appl
182	13	41.9	34	3	US-08-903-497A-4	Sequence 4, Appli

183	13	41.9	34	4	US-09-635-076-4	Sequence 4, Appli
184	13	41.9	35	2	US-08-142-551B-4	Sequence 4, Appli
185	13	41.9	35	2	US-08-142-551B-5	Sequence 5, Appli
186	13	41.9	35	2	US-08-142-551B-7	Sequence 7, Appli
187	13	41.9	35	2	US-08-142-551B-11	Sequence 11, Appl
188	13	41.9	35	2	US-08-142-551B-12	Sequence 12, Appl
189	13	41.9	35	2	US-08-142-551B-13	Sequence 13, Appl
190	13	41.9	35	2	US-08-142-551B-14	Sequence 14, Appl
191	13	41.9	35	2	US-08-142-551B-15	Sequence 15, Appl
192	13	41.9	35	2	US-08-142-551B-16	Sequence 16, Appl
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195	13	41.9	35	2	US-08-142-551B-19	Sequence 19, Appl
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198	13	41.9	35	2	US-08-142-551B-22	Sequence 22, Appl
199	13	41.9	35	2	US-08-142-551B-23	Sequence 23, Appl
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202	13	41.9	35	2	US-08-142-551B-26	Sequence 26, Appl
203	13	41.9	35	2	US-08-142-551B-27	Sequence 27, Appl
204	13	41.9	35	2	US-08-142-551B-28	Sequence 28, Appl
205	13	41.9	35	2	US-08-142-551B-29	Sequence 29, Appl
206	13	41.9	35	2	US-08-142-551B-30	Sequence 30, Appl
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212	13	41.9	35	2	US-08-142-551B-36	Sequence 36, Appl
213	13	41.9	35	2	US-08-142-551B-37	Sequence 37, Appl
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215	13	41.9	35	2	US-08-142-551B-39	Sequence 39, Appl
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218	13	41.9	35	2	US-08-142-551B-42	Sequence 42, Appl
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222	13	41.9	35	2	US-08-142-551B-46	Sequence 46, Appl
223	13	41.9	35	2	US-08-142-551B-47	Sequence 47, Appl
224	13	41.9	35	2	US-08-142-551B-48	Sequence 48, Appl
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229	13	41.9	35	2	US-08-142-551B-53	Sequence 53, Appl
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231	13	41.9	35	2	US-08-142-551B-55	Sequence 55, Appl
232	13	41.9	35	2	US-08-142-551B-56	Sequence 56, Appl
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239	13	41.9	35	2	US-08-142-551B-63	Sequence 63, Appl

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251	13	41.9	35	2	US-08-142-551B-112	Sequence 112, App
252	13	41.9	35	2	US-08-142-551B-113	Sequence 113, App
253	13	41.9	35	2	US-08-142-551B-114	Sequence 114, App
254	13	41.9	35	2	US-08-142-551B-115	Sequence 115, App
255	13	41.9	35	2	US-08-142-551B-116	Sequence 116, App
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257	13	41.9	35	2	US-08-142-551B-118	Sequence 118, App
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259	12	38.7	34	1	US-08-526-987-2	Sequence 2, Appli
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261	12	38.7	35	2	US-08-142-551B-69	Sequence 69, Appl
262	12	38.7	35	2	US-08-142-551B-71	Sequence 71, Appl
263	12	38.7	35	2	US-08-142-551B-107	Sequence 107, App
264	12	38.7	35	2	US-08-142-551B-108	Sequence 108, App
265	12	38.7	35	2	US-08-142-551B-109	Sequence 109, App
266	12	38.7	35	2	US-08-142-551B-110	Sequence 110, App
267	11	35.5	35	2	US-08-142-551B-72	Sequence 72, Appl
268	11	35.5	35	2	US-08-142-551B-74	Sequence 74, Appl
269	11	35.5	35	2	US-08-142-551B-75	Sequence 75, Appl
270	11	35.5	35	2	US-08-142-551B-104	Sequence 104, App
271	11	35.5	35	2	US-08-142-551B-105	Sequence 105, App
272	11	35.5	35	2	US-08-142-551B-106	Sequence 106, App
273	11	35.5	35	2	US-08-142-551B-122	Sequence 122, App
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281	10	32.3	34	4	US-09-635-076-5	Sequence 5, Appli
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284	10	32.3	35	2	US-08-142-551B-78	Sequence 78, Appl
285	10	32.3	35	2	US-08-142-551B-101	Sequence 101, App
286	10	32.3	35	2	US-08-142-551B-102	Sequence 102, App
287	10	32.3	35	2	US-08-142-551B-103	Sequence 103, App
288	10	32.3	35	2	US-08-142-551B-120	Sequence 120, App
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291	9	29.0	28	4	US-09-228-990-65	Sequence 65, Appl
292	9	29.0	28	4	US-09-228-990-79	Sequence 79, Appl
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305	9	29.0	31	4	US-09-228-990-7	Sequence 7, Appli
306	9	29.0	31	4	US-09-228-990-8	Sequence 8, Appli
307	9	29.0	31	4	US-09-228-990-9	Sequence 9, Appli
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325	9	29.0	31	4	US-09-228-990-51	Sequence 51, Appl
326	9	29.0	31	4	US-09-228-990-69	Sequence 69, Appl
327	9	29.0	31	4	US-09-228-990-70	Sequence 70, Appl
328	9	29.0	31	4	US-09-228-990-74	Sequence 74, Appl
329	9	29.0	31	4	US-09-228-990-81	Sequence 81, Appl
330	9	29.0	31	4	US-09-228-990-82	Sequence 82, Appl
331	9	29.0	31	4	US-09-228-990-83	Sequence 83, Appl
332	9	29.0	31	4	US-09-228-990-84	Sequence 84, Appl
333	9	29.0	31	4	US-09-228-990-85	Sequence 85, Appl
334	9	29.0	31	4	US-09-536-785A-13	Sequence 13, Appl
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340	9	29.0	31	4	US-09-442-989-6	Sequence 6, Appli
341	9	29.0	31	4	US-09-442-989-7	Sequence 7, Appli
342	9	29.0	31	4	US-09-442-989-8	Sequence 8, Appli
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344	9	29.0	31	4	US-09-442-989-32	Sequence 32, Appl
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347	9	29.0	34	1	US-08-488-105-17	Sequence 17, Appl
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349	9	29.0	34	1	US-08-449-317A-61	Sequence 61, Appl
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357	9	29.0	34	4	US-09-449-632-22	Sequence 22, Appl
358	9	29.0	34	4	US-09-442-989-18	Sequence 18, Appl
359	9	29.0	34	4	US-09-442-989-46	Sequence 46, Appl
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361	9	29.0	35	2	US-08-142-551B-81	Sequence 81, Appl
362	9	29.0	35	2	US-08-142-551B-82	Sequence 82, Appl
363	9	29.0	35	2	US-08-142-551B-83	Sequence 83, Appl
364	9	29.0	35	2	US-08-142-551B-84	Sequence 84, Appl
365	9	29.0	35	2	US-08-142-551B-85	Sequence 85, Appl
366	9	29.0	35	2	US-08-142-551B-86	Sequence 86, Appl
367	9	29.0	35	2	US-08-142-551B-87	Sequence 87, Appl
368	9	29.0	35	2	US-08-142-551B-88	Sequence 88, Appl
369	9	29.0	35	2	US-08-142-551B-89	Sequence 89, Appl
370	9	29.0	35	2	US-08-142-551B-91	Sequence 91, Appl
371	9	29.0	35	2	US-08-142-551B-92	Sequence 92, Appl
372	9	29.0	35	2	US-08-142-551B-93	Sequence 93, Appl
373	9	29.0	35	2	US-08-142-551B-95	Sequence 95, Appl
374	9	29.0	35	2	US-08-142-551B-96	Sequence 96, Appl
375	9	29.0	35	2	US-08-142-551B-97	Sequence 97, Appl
376	9	29.0	35	2	US-08-142-551B-98	Sequence 98, Appl
377	9	29.0	35	2	US-08-142-551B-99	Sequence 99, Appl
378	9	29.0	35	2	US-08-142-551B-100	Sequence 100, App
379	9	29.0	35	2	US-08-142-551B-121	Sequence 121, App
380	9	29.0	35	2	US-08-142-551B-123	Sequence 123, App
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388	8	25.8	28	4	US-09-442-989-24	Sequence 24, Appl
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395	8	25.8	31	4	US-09-228-990-35	Sequence 35, Appl
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409	8	25.8	34	1	US-07-773-098-4	Sequence 4, Appli
410	8	25.8	34	3	US-08-903-497A-6	Sequence 6, Appli

411	8	25.8	34	4	US-09-635-076-6	Sequence 6, Appli
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413	8	25.8	34	4	US-09-442-989-19	Sequence 19, Appl
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415	8	25.8	36	1	US-07-778-926-19	Sequence 19, Appl
416	8	25.8	37	1	US-07-778-926-8	Sequence 8, Appli
417	8	25.8	38	1	US-07-778-926-12	Sequence 12, Appl
418	8	25.8	39	1	US-07-778-926-16	Sequence 16, Appl
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422	7	22.6	31	4	US-09-228-990-12	Sequence 12, Appl
423	7	22.6	31	4	US-09-228-990-18	Sequence 18, Appl
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425	7	22.6	31	4	US-09-228-990-34	Sequence 34, Appl
426	7	22.6	31	4	US-09-228-990-41	Sequence 41, Appl
427	7	22.6	31	4	US-09-228-990-44	Sequence 44, Appl
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429	7	22.6	31	4	US-09-442-989-15	Sequence 15, Appl
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432	7	22.6	32	1	US-08-305-799A-2	Sequence 2, Appli
433	7	22.6	34	1	US-07-915-247A-23	Sequence 23, Appl
434	7	22.6	34	1	US-07-915-247A-24	Sequence 24, Appl
435	7	22.6	34	1	US-08-443-863-23	Sequence 23, Appl
436	7	22.6	34	1	US-08-443-863-24	Sequence 24, Appl
437	7	22.6	34	1	US-08-448-070-23	Sequence 23, Appl
438	7	22.6	34	1	US-08-448-070-24	Sequence 24, Appl
439	7	22.6	34	1	US-08-468-275-7	Sequence 7, Appli
440	7	22.6	34	1	US-08-468-275-8	Sequence 8, Appli
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443	7	22.6	34	1	US-08-449-500-35	Sequence 35, Appl
444	7	22.6	34	1	US-08-449-500-36	Sequence 36, Appl
445	7	22.6	34	1	US-08-449-317A-23	Sequence 23, Appl
446	7	22.6	34	1	US-08-449-317A-24	Sequence 24, Appl
447	7	22.6	34	1	US-08-449-317A-35	Sequence 35, Appl
448	7	22.6	34	1	US-08-449-317A-36	Sequence 36, Appl
449	7	22.6	34	2	US-08-477-022-23	Sequence 23, Appl
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452	7	22.6	34	2	US-08-477-022-36	Sequence 36, Appl
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454	7	22.6	34	2	US-08-449-447-24	Sequence 24, Appl
455	7	22.6	34	2	US-08-449-447-35	Sequence 35, Appl
456	7	22.6	34	2	US-08-449-447-36	Sequence 36, Appl
457	7	22.6	34	2	US-08-184-328-23	Sequence 23, Appl
458	7	22.6	34	2	US-08-184-328-24	Sequence 24, Appl
459	7	22.6	34	2	US-08-184-328-35	Sequence 35, Appl
460	7	22.6	34	2	US-08-184-328-36	Sequence 36, Appl
461	7	22.6	34	2	US-08-521-097-23	Sequence 23, Appl
462	7	22.6	34	2	US-08-521-097-24	Sequence 24, Appl
463	7	22.6	34	2	US-08-521-097-35	Sequence 35, Appl
464	7	22.6	34	2	US-08-521-097-36	Sequence 36, Appl
465	7	22.6	34	4	US-09-007-466-7	Sequence 7, Appli
466	7	22.6	34	4	US-09-007-466-8	Sequence 8, Appli
467	7	22.6	35	2	US-08-142-551B-10	Sequence 10, Appl

468	7	22.6	35	2	US-08-142-551B-124	Sequence 124, App
469	7	22.6	35	4	US-08-952-980B-7	Sequence 7, Appli
470	7	22.6	35	4	US-08-952-980B-8	Sequence 8, Appli
471	7	22.6	36	1	US-07-778-926-4	Sequence 4, Appli
472	6	19.4	30	4	US-09-536-785A-23	Sequence 23, Appl
473	6	19.4	31	3	US-08-904-760B-23	Sequence 23, Appl
474	6	19.4	31	4	US-09-406-813-7	Sequence 7, Appli
475	6	19.4	31	4	US-09-228-990-13	Sequence 13, Appl
476	6	19.4	31	4	US-09-228-990-14	Sequence 14, Appl
477	6	19.4	31	4	US-09-228-990-15	Sequence 15, Appl
478	6	19.4	31	4	US-09-228-990-16	Sequence 16, Appl
479	6	19.4	31	4	US-09-228-990-17	Sequence 17, Appl
480	6	19.4	31	4	US-09-228-990-30	Sequence 30, Appl
481	6	19.4	31	4	US-09-228-990-31	Sequence 31, Appl
482	6	19.4	31	4	US-09-228-990-32	Sequence 32, Appl
483	6	19.4	31	4	US-09-228-990-33	Sequence 33, Appl
484	6	19.4	31	4	US-09-228-990-42	Sequence 42, Appl
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487	6	19.4	31	4	US-09-228-990-87	Sequence 87, Appl
488	6	19.4	31	4	US-09-228-990-88	Sequence 88, Appl
489	6	19.4	31	4	US-09-536-785A-36	Sequence 36, Appl
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493	6	19.4	31	4	US-09-442-989-13	Sequence 13, Appl
494	6	19.4	31	4	US-09-442-989-14	Sequence 14, Appl
495	6	19.4	32	4	US-09-536-785A-37	Sequence 37, Appl
496	6	19.4	33	4	US-09-536-785A-38	Sequence 38, Appl
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499	6	19.4	34	1	US-08-526-987-1	Sequence 1, Appli
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502	6	19.4	36	4	US-09-536-785A-26	Sequence 26, Appl
503	6	19.4	37	4	US-09-536-785A-27	Sequence 27, Appl
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507	5	16.1	30	1	US-08-305-799A-9	Sequence 9, Appli
508	5	16.1	30	1	US-08-305-799A-10	Sequence 10, Appl
509	5	16.1	30	1	US-08-305-799A-11	Sequence 11, Appl
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512	5	16.1	34	1	US-08-449-317A-37	Sequence 37, Appl
513	5	16.1	34	2	US-08-477-022-37	Sequence 37, Appl
514	5	16.1	34	2	US-08-449-447-37	Sequence 37, Appl
515	5	16.1	34	2	US-08-184-328-37	Sequence 37, Appl
516	5	16.1	34	2	US-08-521-097-37	Sequence 37, Appl
517	5	16.1	38	1	US-08-444-005-19	Sequence 19, Appl
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522	4	12.9	28	2	US-08-818-253-22	Sequence 22, Appl
523	4	12.9	28	3	US-08-641-873-8	Sequence 8, Appli
524	4	12.9	28	3	US-08-818-252-22	Sequence 22, Appl

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529	4	12.9	29	4	US-09-227-357-386	Sequence 386, App
530	4	12.9	29	4	US-09-227-357-480	Sequence 480, App
531	4	12.9	29	4	US-09-695-458-8	Sequence 8, Appli
532	4	12.9	29	4	US-09-205-258-1006	Sequence 1006, Ap
533	4	12.9	30	1	US-08-305-799A-3	Sequence 3, Appli
534	4	12.9	30	1	US-08-305-799A-4	Sequence 4, Appli
535	4	12.9	30	4	US-09-205-258-821	Sequence 821, App
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537	4	12.9	31	1	US-08-340-812-3	Sequence 3, Appli
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541	4	12.9	31	1	US-08-323-531-62	Sequence 62, Appl
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543	4	12.9	31	1	US-08-198-094-50	Sequence 50, Appl
544	4	12.9	31	1	US-08-198-094-62	Sequence 62, Appl
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553	4	12.9	31	3	US-08-107-794A-62	Sequence 62, Appl
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557	4	12.9	31	5	PCT-US93-07424-50	Sequence 50, Appl
558	4	12.9	31	5	PCT-US93-07424-62	Sequence 62, Appl
559	4	12.9	31	5	PCT-US95-02087-44	Sequence 44, Appl
560	4	12.9	31	5	PCT-US95-02087-50	Sequence 50, Appl
561	4	12.9	31	5	PCT-US95-02087-62	Sequence 62, Appl
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564	4	12.9	32	1	US-08-190-802A-114	Sequence 114, App
565	4	12.9	32	1	US-08-190-802A-183	Sequence 183, App
566	4	12.9	32	1	US-08-190-802A-216	Sequence 216, App
567	4	12.9	32	3	US-08-477-346-110	Sequence 110, App
568	4	12.9	32	3	US-08-477-346-114	Sequence 114, App
569	4	12.9	32	3	US-08-477-346-183	Sequence 183, App
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571	4	12.9	32	4	US-08-473-089-110	Sequence 110, App
572	4	12.9	32	4	US-08-473-089-114	Sequence 114, App
573	4	12.9	32	4	US-08-473-089-183	Sequence 183, App
574	4	12.9	32	4	US-08-473-089-216	Sequence 216, App
575	4	12.9	32	4	US-09-149-476-442	Sequence 442, App
576	4	12.9	32	4	US-08-487-072A-110	Sequence 110, App
577	4	12.9	32	4	US-08-487-072A-114	Sequence 114, App
578	4	12.9	32	4	US-08-487-072A-183	Sequence 183, App
579	4	12.9	32	4	US-08-487-072A-216	Sequence 216, App
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586	4	12.9	34	1	US-07-956-700B-7	Sequence 7, Appli
587	4	12.9	34	1	US-08-476-537-7	Sequence 7, Appli
588	4	12.9	34	1	US-08-485-607-7	Sequence 7, Appli
589	4	12.9	34	2	US-08-475-879-7	Sequence 7, Appli
590	4	12.9	34	4	US-09-433-043B-7	Sequence 7, Appli
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592	4	12.9	35	1	US-08-678-280-6	Sequence 6, Appli
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594	4	12.9	35	4	US-09-690-454-138	Sequence 138, App
595	4	12.9	36	1	US-08-477-727A-104	Sequence 104, App
596	4	12.9	36	1	US-08-471-675A-26	Sequence 26, Appl
597	4	12.9	36	2	US-08-892-549-30	Sequence 30, Appl
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600	4	12.9	37	1	US-08-237-418-16	Sequence 16, Appl
601	4	12.9	37	1	US-08-477-727A-102	Sequence 102, App
602	4	12.9	37	1	US-08-477-727A-103	Sequence 103, App
603	4	12.9	37	1	US-08-477-727A-105	Sequence 105, App
604	4	12.9	37	1	US-08-477-727A-106	Sequence 106, App
605	4	12.9	37	1	US-08-477-727A-107	Sequence 107, App
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615	4	12.9	37	2	US-08-505-486-50	Sequence 50, Appl
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621	4	12.9	37	2	US-08-892-549-33	Sequence 33, Appl
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624	4	12.9	37	3	US-09-340-154-50	Sequence 50, Appl
625	4	12.9	37	3	US-08-302-069A-23	Sequence 23, Appl
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628	4	12.9	37	3	US-08-302-069A-27	Sequence 27, Appl
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631	4	12.9	37	3	US-08-468-337-16	Sequence 16, Appl
632	4	12.9	37	4	US-09-482-611B-50	Sequence 50, Appl
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636	4	12.9	37	5	PCT-US95-09339-50	Sequence 50, Appl
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638	4	12.9	38	2	US-08-378-548-12	Sequence 12, Appl

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640	4	12.9	39	4	US-09-323-867A-25	Sequence 25, Appl
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643	3	9.7	28	1	US-07-690-300B-12	Sequence 12, Appl
644	3	9.7	28	1	US-07-690-300B-23	Sequence 23, Appl
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646	3	9.7	28	1	US-07-690-300B-25	Sequence 25, Appl
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665	3	9.7	28	1	US-07-690-300B-44	Sequence 44, Appl
666	3	9.7	28	1	US-07-690-300B-45	Sequence 45, Appl
667	3	9.7	28	1	US-07-690-300B-46	Sequence 46, Appl
668	3	9.7	28	1	US-07-690-300B-47	Sequence 47, Appl
669	3	9.7	28	1	US-07-690-300B-48	Sequence 48, Appl
670	3	9.7	28	1	US-07-690-300B-49	Sequence 49, Appl
671	3	9.7	28	1	US-07-690-300B-50	Sequence 50, Appl
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687	3	9.7	28	1	US-07-690-300B-93	Sequence 93, Appl
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694	3	9.7	28	1	US-07-868-906-1	Sequence 1, Appli
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697	3	9.7	28	1	US-08-055-530-29	Sequence 29, Appl
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699	3	9.7	28	1	US-08-032-848C-1	Sequence 1, Appli
700	3	9.7	28	1	US-07-966-187-2	Sequence 2, Appli
701	3	9.7	28	1	US-08-255-558B-6	Sequence 6, Appli
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705	3	9.7	28	1	US-08-246-572-5	Sequence 5, Appli
706	3	9.7	28	1	US-08-190-802A-84	Sequence 84, Appl
707	3	9.7	28	1	US-08-361-443-1	Sequence 1, Appli
708	3	9.7	28	1	US-08-311-611A-12	Sequence 12, Appl
709	3	9.7	28	1	US-08-311-611A-56	Sequence 56, Appl
710	3	9.7	28	1	US-08-311-611A-193	Sequence 193, App
711	3	9.7	28	1	US-08-311-611A-194	Sequence 194, App
712	3	9.7	28	1	US-08-311-611A-195	Sequence 195, App
713	3	9.7	28	1	US-08-311-611A-196	Sequence 196, App
714	3	9.7	28	1	US-07-938-782A-8	Sequence 8, Appli
715	3	9.7	28	1	US-07-949-797B-1	Sequence 1, Appli
716	3	9.7	28	1	US-08-194-591-1	Sequence 1, Appli
717	3	9.7	28	1	US-08-194-591-2	Sequence 2, Appli
718	3	9.7	28	1	US-08-257-446-6	Sequence 6, Appli
719	3	9.7	28	1	US-08-372-783-12	Sequence 12, Appl
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722	3	9.7	28	1	US-08-372-783-194	Sequence 194, App
723	3	9.7	28	1	US-08-372-783-195	Sequence 195, App
724	3	9.7	28	1	US-08-372-783-196	Sequence 196, App
725	3	9.7	28	1	US-07-794-288D-7	Sequence 7, Appli
726	3	9.7	28	1	US-07-794-288D-65	Sequence 65, Appl
727	3	9.7	28	1	US-07-794-288D-103	Sequence 103, App
728	3	9.7	28	1	US-07-977-630-42	Sequence 42, Appl
729	3	9.7	28	1	US-07-977-630-45	Sequence 45, Appl
730	3	9.7	28	1	US-07-977-630-47	Sequence 47, Appl
731	3	9.7	28	1	US-08-288-681A-1	Sequence 1, Appli
732	3	9.7	28	1	US-08-366-591-12	Sequence 12, Appl
733	3	9.7	28	1	US-07-776-272-26	Sequence 26, Appl
734	3	9.7	28	1	US-08-372-105-12	Sequence 12, Appl
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ALIGNMENTS

RESULT 1

US-08-262-495C-3

; Sequence 3, Application US/08262495C

; Patent No. 5556940

; GENERAL INFORMATION:

; APPLICANT: WILICK, Gordon E.

; APPLICANT: WHITFIELD, James F.

; APPLICANT: SUREWICZ, Witold

; APPLICANT: SUNG, Wing L.

; APPLICANT: NEUGENBAUER, Witold

; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 6

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Kirby, Eades, Gale, Baker

; STREET: 112 Kent Street, Suite 770,

; CITY: Ottawa

; COUNTRY: Canada

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC Compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Wordperfect 5.1

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/262,495C

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; CLASSIFICATION: 530

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; APPLICATION NUMBER:

; FILING DATE:

; CLASSIFICATION: 530

; ATTORNEY/AGENT INFORMATION:

; TELEFAX: (703) 816-4100
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; TOPOLOGY: cyclic
; MOLECULE TYPE: protein
US-08-691-647C-6

Query Match 100.0%; Score 31; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 4

US-08-904-760B-1

; Sequence 1, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000

; TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 31 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-904-760B-1

Query Match 100.0%; Score 31; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 5

US-08-904-760B-6

; Sequence 6, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/904,760B
; FILING DATE: 01-AUG-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/691,647
; FILING DATE: 02-AUG-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Crawford, Arthur R.
; REGISTRATION NUMBER: 25,327
; REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-816-4000

; TELEFAX: 703-816-4100
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 31 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: circular
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; OTHER INFORMATION: cyclo Lys27-Asp30, and this sequence
 ; OTHER INFORMATION: has an amino group c-terminus (NH2).
 US-08-904-760B-6

Query Match 100.0%; Score 31; DB 3; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.4e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 6

US-08-904-760B-14

; Sequence 14, Application US/08904760B
 ; Patent No. 6110892
 ; GENERAL INFORMATION:
 ; APPLICANT: Jean-Rene, Barbier
 ; APPLICANT: Neugebauer, Witold
 ; APPLICANT: Ross, Virginia
 ; APPLICANT: Whitfield, James
 ; APPLICANT: Willick, Gordon E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
 ; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
 ; NUMBER OF SEQUENCES: 35
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: NIXON & VANDERHYE P.C.
 ; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
 ; CITY: Arlington
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22201-4741
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/904,760B
 ; FILING DATE: 01-AUG-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/691,647
 ; FILING DATE: 02-AUG-1996
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Crawford, Arthur R.
 ; REGISTRATION NUMBER: 25,327


```

; ATTORNEY/AGENT INFORMATION:
;   NAME: Crawford, Arthur R.
;   REGISTRATION NUMBER: 25,327
;   REFERENCE/DOCKET NUMBER: 1339-6
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 703-816-4000
;   TELEFAX: 703-816-4100
; INFORMATION FOR SEQ ID NO: 32:
;   SEQUENCE CHARACTERISTICS:
;     LENGTH: 31 amino acids
;     TYPE: amino acid
;     STRANDEDNESS:
;     TOPOLOGY: linear
;   MOLECULE TYPE: protein
;   FEATURE:
;     OTHER INFORMATION: This sequence has an amino group
;     OTHER INFORMATION: c-terminus (NH2).
US-08-904-760B-32

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```

Query Match          100.0%; Score 31; DB 3; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 8

```

US-09-406-813-2
; Sequence 2, Application US/09406813
; Patent No. 6316410
; GENERAL INFORMATION:
;   APPLICANT: Barbier, Jean-Rene
;   APPLICANT: Morley, Paul
;   APPLICANT: Whitfield, James
;   APPLICANT: Willick, Gordon E.
;   TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
;   TITLE OF INVENTION: OSTEOPOROSIS
;   FILE REFERENCE: 10688-1B
;   CURRENT APPLICATION NUMBER: US/09/406,813
;   CURRENT FILING DATE: 1999-09-22
;   PRIOR APPLICATION NUMBER: 08/904,760
;   PRIOR FILING DATE: 1997-08-01
;   NUMBER OF SEQ ID NOS: 9
;   SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;     OTHER INFORMATION: This sequence has an amino group c-terminus (NH2).
US-09-406-813-2

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```

Query Match          100.0%; Score 31; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 9

US-09-536-785A-1
 ; Sequence 1, Application US/09536785A
 ; Patent No. 6541450
 ; GENERAL INFORMATION:
 ; APPLICANT: BARBIER, JEAN-RENE
 ; APPLICANT: MORLEY, PAUL
 ; APPLICANT: NEUGEBAUER, WITOLD
 ; APPLICANT: ROSS, VIRGINIA J.S.
 ; APPLICANT: WHITFIELD, JAMES F.
 ; APPLICANT: WILICK, GORDON E.
 ; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
 ; TITLE OF INVENTION: OSTEOPOROSIS
 ; FILE REFERENCE: 1339-9
 ; CURRENT APPLICATION NUMBER: US/09/536,785A
 ; CURRENT FILING DATE: 2000-03-28
 ; PRIOR APPLICATION NUMBER: 08/904,760
 ; PRIOR FILING DATE: 1997-08-01
 ; PRIOR APPLICATION NUMBER: 08/691,647
 ; PRIOR FILING DATE: 1996-08-02
 ; PRIOR APPLICATION NUMBER: 08/262,495
 ; PRIOR FILING DATE: 1994-06-20
 ; PRIOR APPLICATION NUMBER: 60/040,560
 ; PRIOR FILING DATE: 1997-03-14
 ; NUMBER OF SEQ ID NOS: 39
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-536-785A-1

Query Match 100.0%; Score 31; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 4.4e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 10

US-09-536-785A-6
 ; Sequence 6, Application US/09536785A
 ; Patent No. 6541450
 ; GENERAL INFORMATION:
 ; APPLICANT: BARBIER, JEAN-RENE
 ; APPLICANT: MORLEY, PAUL
 ; APPLICANT: NEUGEBAUER, WITOLD
 ; APPLICANT: ROSS, VIRGINIA J.S.
 ; APPLICANT: WHITFIELD, JAMES F.

```

; APPLICANT:  WILLOCK, GORDON E.
; TITLE OF INVENTION:  PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION:  OSTEOPOROSIS
; FILE REFERENCE:  1339-9
; CURRENT APPLICATION NUMBER:  US/09/536,785A
; CURRENT FILING DATE:  2000-03-28
; PRIOR APPLICATION NUMBER:  08/904,760
; PRIOR FILING DATE:  1997-08-01
; PRIOR APPLICATION NUMBER:  08/691,647
; PRIOR FILING DATE:  1996-08-02
; PRIOR APPLICATION NUMBER:  08/262,495
; PRIOR FILING DATE:  1994-06-20
; PRIOR APPLICATION NUMBER:  60/040,560
; PRIOR FILING DATE:  1997-03-14
; NUMBER OF SEQ ID NOS:  39
; SOFTWARE:  PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH:  31
;   TYPE:  PRT
;   ORGANISM:  Homo sapiens
;   FEATURE:
;   NAME/KEY:  SITE
;   LOCATION:  (27)..(30)
;   OTHER INFORMATION:  Cyclo Lys27-Asp30
;   OTHER INFORMATION:  Amino c-terminus
US-09-536-785A-6

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Query Match          100.0%;  Score 31;  DB 4;  Length 31;
Best Local Similarity 100.0%;  Pred. No. 4.4e-22;
Matches   31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

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RESULT 11

```

US-09-536-785A-14
; Sequence 14, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT:  BARBIER, JEAN-RENE
; APPLICANT:  MORLEY, PAUL
; APPLICANT:  NEUGEBAUER, WITOLD
; APPLICANT:  ROSS, VIRGINIA J.S.
; APPLICANT:  WHITFIELD, JAMES F.
; APPLICANT:  WILLOCK, GORDON E.
; TITLE OF INVENTION:  PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION:  OSTEOPOROSIS
; FILE REFERENCE:  1339-9
; CURRENT APPLICATION NUMBER:  US/09/536,785A
; CURRENT FILING DATE:  2000-03-28
; PRIOR APPLICATION NUMBER:  08/904,760
; PRIOR FILING DATE:  1997-08-01
; PRIOR APPLICATION NUMBER:  08/691,647
; PRIOR FILING DATE:  1996-08-02
; PRIOR APPLICATION NUMBER:  08/262,495

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```
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (22)..(26)
; OTHER INFORMATION: Cyclo Glu22-Lys26
; OTHER INFORMATION: Amino c-terminus
US-09-536-785A-14
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Query Match          100.0%; Score 31; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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RESULT 12

US-09-536-785A-32

```
; Sequence 32, Application US/09536785A
; Patent No. 6541450
; GENERAL INFORMATION:
; APPLICANT: BARBIER, JEAN-RENE
; APPLICANT: MORLEY, PAUL
; APPLICANT: NEUGEBAUER, WITOLD
; APPLICANT: ROSS, VIRGINIA J.S.
; APPLICANT: WHITFIELD, JAMES F.
; APPLICANT: WILLICK, GORDON E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 1339-9
; CURRENT APPLICATION NUMBER: US/09/536,785A
; CURRENT FILING DATE: 2000-03-28
; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; PRIOR APPLICATION NUMBER: 08/691,647
; PRIOR FILING DATE: 1996-08-02
; PRIOR APPLICATION NUMBER: 08/262,495
; PRIOR FILING DATE: 1994-06-20
; PRIOR APPLICATION NUMBER: 60/040,560
; PRIOR FILING DATE: 1997-03-14
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 32
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Amino c-terminus
```

US-09-536-785A-32

Query Match 100.0%; Score 31; DB 4; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.4e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 13

US-09-447-800-9

; Sequence 9, Application US/09447800
; Patent No. 6537965
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630001
; CURRENT APPLICATION NUMBER: US/09/447,800
; CURRENT FILING DATE: 1999-11-23
; EARLIER APPLICATION NUMBER: 60/110,152
; EARLIER FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser

US-09-447-800-9

Query Match 100.0%; Score 31; DB 4; Length 33;
Best Local Similarity 100.0%; Pred. No. 4.6e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 14

US-07-765-373-1

; Sequence 1, Application US/07765373
; Patent No. 5393869
; GENERAL INFORMATION:
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: KAWASE, Masahiro
; APPLICANT: YAMAZAKI, Iwao
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES

```

; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/765,373
; FILING DATE: 19910925
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, Gregory D.
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 41289
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; TELEX: 20091 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
US-07-765-373-1

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```

Query Match          100.0%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 15

US-08-033-099-1

```

; Sequence 1, Application US/08033099
; Patent No. 5434246

```

GENERAL INFORMATION:

```

; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DAVID G.CONLIN; DIKE, BRONSTEIN, ROBERTS &
; ADDRESSEE: CUSHMAN

```

```

; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/033,099
; FILING DATE: 19930316
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: WILLIAMS, Gregory D
; REGISTRATION NUMBER: 30901
; REFERENCE/DOCKET NUMBER: 42528
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (613)523-6440
; TELEX: 200291 STRE UR
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-033-099-1

```

```

Query Match          100.0%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

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RESULT 16

US-08-262-495C-1

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; Sequence 1, Application US/08262495C
; Patent No. 5556940
; GENERAL INFORMATION:
; APPLICANT: WILLICK, Gordon E.
; APPLICANT: WHITFIELD, James F.
; APPLICANT: SUREWICZ, Witold
; APPLICANT: SUNG, Wing L.
; APPLICANT: NEUGENBAUER, Witold
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kirby, Eades, Gale, Baker
; STREET: 112 Kent Street, Suite 770,
; CITY: Ottawa

```

```

; COUNTRY: Canada
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/262,495C
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: EADES, No. 5556940ris M.
; REGISTRATION NUMBER: 5,263
; REFERENCE/DOCKET NUMBER: 36210
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (613)-237-6900
; TELEFAX: (613)-237-0045
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-262-495C-1

```

```

Query Match          100.0%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 17

US-07-915-247A-1

; Sequence 1, Application US/07915247A

; Patent No. 5589452

; GENERAL INFORMATION:

; APPLICANT: Krstenansky, John L.

; APPLICANT: Nestor Jr., John J.

; APPLICANT: Ho, Teresa H.

; APPLICANT: Vickery, Brian H.

; APPLICANT: Bach, Chinh T.

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND

; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE

; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

; NUMBER OF SEQUENCES: 34

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.

; STREET: 3401 Hillview Ave.

; CITY: Palo Alto

; STATE: CA

```

; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/915,247A
; FILING DATE: 19920714
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-07-915-247A-1

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Query Match          100.0%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

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RESULT 18

US-08-443-863-1

```

; Sequence 1, Application US/08443863
; Patent No. 5693616

```

GENERAL INFORMATION:

```

; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA

```

```

; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/443,863
; FILING DATE: 14-JUL-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-443-863-1

```

```

Query Match          100.0%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

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```

RESULT 19
US-08-448-070-1
; Sequence 1, Application US/08448070
; Patent No. 5695955
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 34
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

```

```

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/448,070
; FILING DATE: 14-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-448-070-1

```

```

Query Match          100.0%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

```

RESULT 20
US-08-488-105-7
; Sequence 7, Application US/08488105
; Patent No. 5717062
; GENERAL INFORMATION:
; APPLICANT: Chorev, Michael
; APPLICANT: Rosenblatt, Michael
; TITLE OF INVENTION: CYCLIC ANALOGS OF PTH AND PTHrP
; NUMBER OF SEQUENCES: 22
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

```


; APPLICATION NUMBER: US/08/488,105
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Tsao, Y. Rocky
 ; REGISTRATION NUMBER: 34,053
 ; REFERENCE/DOCKET NUMBER: 00537/112001
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 617/542-5070
 ; TELEFAX: 617/542-8906
 ; TELEX: 200154
 ; INFORMATION FOR SEQ ID NO: 7:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; FEATURE:
 ; OTHER INFORMATION: The side chains of Lys at
 ; OTHER INFORMATION: position 26 and Asp at position 30 are linked by an
 amide bond,
 ; OTHER INFORMATION: and this sequence has an amide C-terminus (i.e.,
 CONH2), rather
 ; OTHER INFORMATION: than a carboxy C-terminus (i.e., COOH).
 US-08-488-105-7

Query Match 100.0%; Score 31; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.7e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 ||||||||||||||||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 21

US-08-468-275-6

; Sequence 6, Application US/08468275
 ; Patent No. 5747453
 ; GENERAL INFORMATION:
 ; APPLICANT: HOLLADAY, LESLIE A.
 ; APPLICANT: OLDENBURG, KEVIN R.
 ; TITLE OF INVENTION: METHOD FOR INCREASING THE
 ; TITLE OF INVENTION: ELECTROTRANSPORT FLUX OF POLYPEPTIDES
 ; NUMBER OF SEQUENCES: 10
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ALZA CORPORATION
 ; STREET: 950 PAGE MILL ROAD
 ; CITY: PALO ALTO
 ; STATE: CALIFORNIA
 ; COUNTRY: USA
 ; ZIP: 94303-0802
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS

```

;   SOFTWARE: PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/468,275
;   FILING DATE: 06-JUN-1995
;   CLASSIFICATION: 514
;   ATTORNEY/AGENT INFORMATION:
;   NAME: MILLER, D. BYRON
;   REGISTRATION NUMBER: 30,661
;   REFERENCE/DOCKET NUMBER: O360-0002; ARC-2349
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (415) 496-8150
;   TELEFAX: (415) 496-8048
;   INFORMATION FOR SEQ ID NO: 6:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 34 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-468-275-6

```

```

Query Match          100.0%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 22

US-08-449-500-1

```

; Sequence 1, Application US/08449500
; Patent No. 5798225

```

GENERAL INFORMATION:

```

;   APPLICANT: Krstenansky, John L.
;   APPLICANT: Nestor Jr., John J.
;   APPLICANT: Ho, Teresa H.
;   APPLICANT: Vickery, Brian H.
;   APPLICANT: Bach, Chinh T.
;   TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
;   TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
;   TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
;   NUMBER OF SEQUENCES: 86
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
;   STREET: 3401 Hillview Ave.
;   CITY: Palo Alto
;   STATE: CA
;   COUNTRY: USA
;   ZIP: 94303
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:

```

; APPLICATION NUMBER: US/08/449,500
 ; FILING DATE: 18-JAN-1994
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Schmonsees, William
 ; REGISTRATION NUMBER: 31,796
 ; REFERENCE/DOCKET NUMBER: 27610-P1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 415-855-6593
 ; TELEFAX: 415-496-3529
 ; INFORMATION FOR SEQ ID NO: 1:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 34 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; HYPOTHETICAL: NO
 ; FRAGMENT TYPE: N-terminal
 US-08-449-500-1

Query Match 100.0%; Score 31; DB 1; Length 34;
 Best Local Similarity 100.0%; Pred. No. 4.7e-22;
 Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 23

US-08-449-317A-1

; Sequence 1, Application US/08449317A
 ; Patent No. 5807823

; GENERAL INFORMATION:

; APPLICANT: Vickery, Brian H.
 ; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
 ; TITLE OF INVENTION: INDUCED OSTEOPENIA
 ; NUMBER OF SEQUENCES: 86
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
 ; STREET: 3401 Hillview Ave.
 ; CITY: Palo Alto
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94303

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/449,317A
 ; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Schmonsees, William
 ; REGISTRATION NUMBER: 31,796

```

; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-317A-1

```

```

Query Match          100.0%; Score 31; DB 1; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 24

US-08-142-551B-2

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; Sequence 2, Application US/08142551B
; Patent No. 5814603
; GENERAL INFORMATION:
; APPLICANT: Oldenburg, Kevin R.
; APPLICANT: Selick, Harold E.
; TITLE OF INVENTION: COMPOUNDS WITH PTH ACTIVITY AND
; TITLE OF INVENTION: RECOMBINANT DNA VECTORS ENCODING SAME
; NUMBER OF SEQUENCES: 132
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burns, Doane, Swecker & Mathis
; STREET: 699 Prince Street
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: US
; ZIP: 22313
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/142,551B
; FILING DATE: 25-OCT-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/077,296
; FILING DATE: 14-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/898,219
; FILING DATE: 12-JUN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/965,677

```

```

; FILING DATE: 22-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Swiss, Gerald F.
; REGISTRATION NUMBER: 30,113
; REFERENCE/DOCKET NUMBER: 000324-010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 854-7400
; TELEFAX: (415) 854-8275
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "The sequence of the 34
; OTHER INFORMATION: amino acid truncated human PTH peptide,
; OTHER INFORMATION: designated: Human PTH."

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US-08-142-551B-2

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Query Match          100.0%; Score 31; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 25

US-08-477-022-1

```

; Sequence 1, Application US/08477022
; Patent No. 5821225
; GENERAL INFORMATION:
; APPLICANT: Vickery, Brian H.
; TITLE OF INVENTION: METHOD FOR TREATMENT OF CORTICOSTEROID
; TITLE OF INVENTION: INDUCED OSTEOPENIA
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/477,022
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:

```

; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-477-022-1

Query Match 100.0%; Score 31; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
| | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 26

US-08-449-447-1

; Sequence 1, Application US/08449447
; Patent No. 5840837
; GENERAL INFORMATION:
; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.
; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,447
; FILING DATE: 18-JAN-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William

; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-449-447-1

Query Match 100.0%; Score 31; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
| | | | | | | | | | | | | | | | | | | | | | | | | |
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 27

US-08-835-231-13

; Sequence 13, Application US/08835231

; Patent No. 5861284

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 5861284uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

; COMPUTER: IBM Compatible

; OPERATING SYSTEM: DOS

; SOFTWARE: FastSEQ Version 1.5

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/835,231

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/350,709

; FILING DATE: 07-DEC-1994

; APPLICATION NUMBER: 07/838,857

; FILING DATE: 18-FEB-1992

```

; APPLICATION NUMBER: JP 024841
; FILING DATE: 19-FEB-1991
; APPLICATION NUMBER: JP 0271438
; FILING DATE: 18-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: DAVID, RESNICK S
; REGISTRATION NUMBER: 34,235
; REFERENCE/DOCKET NUMBER: 41614-FWC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-523-3400
; TELEFAX: 617-523-6440
; TELEX: 200291 STRE
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
US-08-835-231-13

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```

Query Match          100.0%; Score 31; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 28

US-08-184-328-1

```

; Sequence 1, Application US/08184328
; Patent No. 5874086

```

GENERAL INFORMATION:

```

; APPLICANT: Krstenansky, John L.
; APPLICANT: Nestor Jr., John J.
; APPLICANT: Ho, Teresa H.
; APPLICANT: Vickery, Brian H.
; APPLICANT: Bach, Chinh T.

```

```

; TITLE OF INVENTION: ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION: PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS

```

NUMBER OF SEQUENCES: 86

CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: Patent Dept., Syntex (U.S.A.), Inc.
; STREET: 3401 Hillview Ave.
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94303

```

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk


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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  PatentIn Release #1.0, Version #1.25
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/184,328
;      FILING DATE:  18-JAN-1994
;      CLASSIFICATION:  435
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Schmonsees, William
;      REGISTRATION NUMBER:  31,796
;      REFERENCE/DOCKET NUMBER:  27610-P1
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  415-855-6593
;      TELEFAX:  415-496-3529
;      INFORMATION FOR SEQ ID NO:  1:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
;      HYPOTHETICAL:  NO
;      FRAGMENT TYPE:  N-terminal
US-08-184-328-1

```

```

Query Match          100.0%;  Score 31;  DB 2;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 4.7e-22;
Matches   31;  Conservative    0;  Mismatches    0;  Indels      0;  Gaps      0;

```

```

Qy      1  SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
          ||||||||||||||||||||||||||||
Db      1  SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

```

RESULT 29
US-08-411-726-2
; Sequence 2, Application US/08411726
; Patent No. 5880093
; GENERAL INFORMATION:
; APPLICANT:  BAGNOLI, Franco
; TITLE OF INVENTION:  Use of Parathormone, Its Biologically
; TITLE OF INVENTION:  Active Fragments and Correlated Peptides, for The
Preparation of
; TITLE OF INVENTION:  Pharmaceutical Compositions Useful for The Treatment
of Pregnanc
; NUMBER OF SEQUENCES:  5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Kenyon & Kenyon
; STREET:  1 Broadway
; CITY:  New York
; STATE:  NY
; COUNTRY:  US
; ZIP:  10004
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  3.5 Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS 6.2
; SOFTWARE:  WordPerfect 6.1 for Windows

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/411,726
; FILING DATE: 05-APR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/02755
; FILING DATE: 08-OCT-1993
; APPLICATION NUMBER: MI-92A002331
; FILING DATE: 09-OCT-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: PALMESE, Maria Luisa
; REGISTRATION NUMBER: 34,402
; REFERENCE/DOCKET NUMBER: 2111/1300
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-425-7200
; TELEFAX: 212-425-5288
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-411-726-2

```

```

Query Match          100.0%; Score 31; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

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RESULT 30

US-08-691-647C-5

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; Sequence 5, Application US/08691647C
; Patent No. 5955425

```

; GENERAL INFORMATION:

```

; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.

```

```

; TITLE OF INVENTION: CYCLIC PARATHYROID HORMONE ANALOGUES
; TITLE OF INVENTION: FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 6

```

; CORRESPONDENCE ADDRESS:

```

; ADDRESSEE: NIXON & VANDERHYE, P.C.
; STREET: 1100 New York Avenue, 8th Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22201-4714

```

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk

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;      COMPUTER:  IBM PC compatible
;      OPERATING SYSTEM:  PC-DOS/MS-DOS
;      SOFTWARE:  ASCII Text
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/08/691,647C
;      FILING DATE:  August 2, 1996
;      CLASSIFICATION:  514
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  Crawford, Arthur R.
;      REGISTRATION NUMBER:  25,327
;      REFERENCE/DOCKET NUMBER:  1339-5
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  (703) 816-4005
;      TELEFAX:  (703) 816-4100
;      TELEX:  N/A
;      INFORMATION FOR SEQ ID NO:  5:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  protein
US-08-691-647C-5

```

```

Query Match          100.0%;  Score 31;  DB 2;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 4.7e-22;
Matches  31;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

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RESULT 31

US-08-521-097-1

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; Sequence 1, Application US/08521097
; Patent No. 5977070
; GENERAL INFORMATION:
; APPLICANT:  Krstenansky, John L.
; APPLICANT:  Nestor Jr., John J.
; APPLICANT:  Ho, Teresa H.
; APPLICANT:  Vickery, Brian H.
; APPLICANT:  Bach, Chinh T.
; TITLE OF INVENTION:  ANALOGS OF PARATHYROID HORMONE AND
; TITLE OF INVENTION:  PARATHYROID HORMONE RELATED PEPTIDE: SYNTHESIS AND USE
; TITLE OF INVENTION:  FOR THE TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES:  86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE:  Patent Dept., Syntex (U.S.A.), Inc.
; STREET:  3401 Hillview Ave.
; CITY:  Palo Alto
; STATE:  CA
; COUNTRY:  USA
; ZIP:  94303
; COMPUTER READABLE FORM:
; MEDIUM TYPE:  Floppy disk
; COMPUTER:  IBM PC compatible
; OPERATING SYSTEM:  PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/521,097
; FILING DATE: 29-AUG-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/184,328
; FILING DATE: 18-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Schmonsees, William
; REGISTRATION NUMBER: 31,796
; REFERENCE/DOCKET NUMBER: 27610-P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-6593
; TELEFAX: 415-496-3529
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; FRAGMENT TYPE: N-terminal
US-08-521-097-1

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Query Match          100.0%; Score 31; DB 2; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

```

RESULT 32
US-09-044-536A-1
; Sequence 1, Application US/09044536A
; Patent No. 6025467
; GENERAL INFORMATION:
; APPLICANT: FUKUDA, Tsunehiko
; APPLICANT: NAKAGAWA, Shizue
; APPLICANT: HABASHITA, Junko
; APPLICANT: TAKETOMI, Shigehisa
; TITLE OF INVENTION: PARATHYROID HORMONE DERIVATIVES AND THEIR USE
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN
; STREET: 130 Water Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: US
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/044,536A
; FILING DATE: 19-MAR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/662,871
; FILING DATE: 12-JUN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: CONLIN, David G
; REGISTRATION NUMBER: 27,026
; REFERENCE/DOCKET NUMBER: 46509-DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)523-3400
; TELEFAX: (617)523-6440
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: partial peptide
; LOCATION: 1..34
US-09-044-536A-1

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Query Match          100.0%; Score 31; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

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RESULT 33
US-08-904-760B-22
; Sequence 22, Application US/08904760B
; Patent No. 6110892
; GENERAL INFORMATION:
; APPLICANT: Jean-Rene, Barbier
; APPLICANT: Neugebauer, Witold
; APPLICANT: Ross, Virginia
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE
; TITLE OF INVENTION: TREATMENT OF OSTEOPOROSIS
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: NIXON & VANDERHYE P.C.
; STREET: 1100 No. 6110892th Glebe Rd. 8th floor
; CITY: Arlington
; STATE: VA
; COUNTRY: USA
; ZIP: 22201-4741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

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;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER:  US/08/904,760B
;   FILING DATE:  01-AUG-1997
;   CLASSIFICATION:  514
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER:  08/691,647
;   FILING DATE:  02-AUG-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME:  Crawford, Arthur R.
;   REGISTRATION NUMBER:  25,327
;   REFERENCE/DOCKET NUMBER:  1339-6
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE:  703-816-4000
;   TELEFAX:  703-816-4100
;   INFORMATION FOR SEQ ID NO:  22:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH:  34 amino acids
;   TYPE:  amino acid
;   STRANDEDNESS:
;   TOPOLOGY:  linear
;   MOLECULE TYPE:  protein
US-08-904-760B-22

```

```

Query Match          100.0%;  Score 31;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 4.7e-22;
Matches  31;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 34

US-08-903-497A-1

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; Sequence 1, Application US/08903497A
; Patent No. 6147186
;   GENERAL INFORMATION:
;   APPLICANT:  Gardella, Thomas J.
;   APPLICANT:  J ppner, Harald
;   TITLE OF INVENTION:  No. 6147186el Parathyroid Hormone-Related
;   TITLE OF INVENTION:  Peptide Analogs
;   NUMBER OF SEQUENCES:  7
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE:  Sterne, Kessler, Goldstein and Fox P.L.L.C.
;   STREET:  1100 New York Avenue, N.W., Suite 600
;   CITY:  Washington
;   STATE:  DC
;   COUNTRY:  USA
;   ZIP:  20005
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE:  Floppy disk
;   COMPUTER:  IBM PC compatible
;   OPERATING SYSTEM:  PC-DOS/MS-DOS
;   SOFTWARE:  PatentIn Release #1.0, Version #1.30
;   CURRENT APPLICATION DATA:

```

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; APPLICATION NUMBER: US/08/903,497A
; FILING DATE: 30-JUL-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/025,471
; FILING DATE: 31-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Markowicz, Karen R.
; REGISTRATION NUMBER: 36,351
; REFERENCE/DOCKET NUMBER: 0609.4310001/JAG/KRM
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 371-2600
; TELEFAX: (202) 371-2540
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: MODIFIED-SITE
; LOCATION: 34
; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
; OTHER INFORMATION: AMIDE
US-08-903-497A-1

```

```

Query Match          100.0%; Score 31; DB 3; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 35

US-09-108-661-13

; Sequence 13, Application US/09108661

; Patent No. 6287806

; GENERAL INFORMATION:

; APPLICANT: NISHIMURA, Osamu

; APPLICANT: KURIYAMA, Masato

; APPLICANT: KOYAMA, No. 6287806uyuki

; APPLICANT: FUKUDA, Tsunehiko

; TITLE OF INVENTION: METHOD FOR PRODUCING A BIOLOGICALLY

; TITLE OF INVENTION: ACTIVE RECOMBINANT CYSTEINE-FREE

; NUMBER OF SEQUENCES: 37

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP

; STREET: 130 WATER STREET

; CITY: BOSTON

; STATE: MA

; COUNTRY: USA

; ZIP: 02109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Diskette

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;      COMPUTER:  IBM Compatible
;      OPERATING SYSTEM:  DOS
;      SOFTWARE:  FastSEQ Version 1.5
;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:  US/09/108,661
;      FILING DATE:
;      CLASSIFICATION:  435
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER:  08/350,709
;      FILING DATE:  07-DEC-1994
;      APPLICATION NUMBER:  07/838,857
;      FILING DATE:  18-FEB-1992
;      APPLICATION NUMBER:  JP 024841
;      FILING DATE:  19-FEB-1991
;      APPLICATION NUMBER:  JP 0271438
;      FILING DATE:  18-OCT-1991
;      ATTORNEY/AGENT INFORMATION:
;      NAME:  DAVID, RESNICK S
;      REGISTRATION NUMBER:  34,235
;      REFERENCE/DOCKET NUMBER:  41614-FWC
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE:  617-523-3400
;      TELEFAX:  617-523-6440
;      TELEX:  200291 STRE
;      INFORMATION FOR SEQ ID NO:  13:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:  34 amino acids
;      TYPE:  amino acid
;      STRANDEDNESS:  single
;      TOPOLOGY:  linear
;      MOLECULE TYPE:  peptide
;      HYPOTHETICAL:  NO
;      ANTI-SENSE:  NO
;      FRAGMENT TYPE:  N-terminal
;      ORIGINAL SOURCE:
US-09-108-661-13

```

```

Query Match          100.0%;  Score 31;  DB 3;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 4.7e-22;
Matches   31;  Conservative   0;  Mismatches   0;  Indels   0;  Gaps   0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

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RESULT 36

US-09-007-466-6

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; Sequence 6, Application US/09007466
; Patent No. 6313092
; GENERAL INFORMATION:
; APPLICANT:  HOLLADAY, LESLIE A.
; APPLICANT:  OLDENBURG, KEVIN R.
; TITLE OF INVENTION:  METHOD FOR INCREASING THE
; TITLE OF INVENTION:  ELECTROTRANSPORT FLUX OF POLYPEPTIDES
; NUMBER OF SEQUENCES:  10
; CORRESPONDENCE ADDRESS:

```



```

; ADDRESSEE: ALZA CORPORATION
; STREET: 950 PAGE MILL ROAD
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94303-0802
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/007,466
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/468,275
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: MILLER, D. BYRON
; REGISTRATION NUMBER: 30,661
; REFERENCE/DOCKET NUMBER: 0360-0002; ARC-2349
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 496-8150
; TELEFAX: (415) 496-8048
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-007-466-6

```

```

Query Match          100.0%; Score 31; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

```

RESULT 37
US-09-406-813-1
; Sequence 1, Application US/09406813
; Patent No. 6316410
; GENERAL INFORMATION:
; APPLICANT: Barbier, Jean-Rene
; APPLICANT: Morley, Paul
; APPLICANT: Whitfield, James
; APPLICANT: Willick, Gordon E.
; TITLE OF INVENTION: PARATHYROID HORMONE ANALOGUES FOR THE TREATMENT OF
; TITLE OF INVENTION: OSTEOPOROSIS
; FILE REFERENCE: 10688-1B
; CURRENT APPLICATION NUMBER: US/09/406,813
; CURRENT FILING DATE: 1999-09-22

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; PRIOR APPLICATION NUMBER: 08/904,760
; PRIOR FILING DATE: 1997-08-01
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
;   LENGTH: 34
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-406-813-1
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Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLODV 31

; NAME/KEY: MODIFIED-SITE
; LOCATION: 34
; OTHER INFORMATION: CARBOXY-TERMINAL MODIFICATION OF TYROSINE-
; OTHER INFORMATION: AMIDE
US-09-635-076-1

Query Match 100.0%; Score 31; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 40

US-09-228-990-1

; Sequence 1, Application US/09228990
; Patent No. 6472505
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; APPLICANT: Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/228,990
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide

; FRAGMENT TYPE: N-terminal
US-09-228-990-1

Query Match 100.0%; Score 31; DB 4; Length 34;
Best Local Similarity 100.0%; Pred. No. 4.7e-22;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
||||||||||||||||||||||||||||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Search completed: January 14, 2004, 10:43:34
Job time : 12.5265 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 9.17445 Seconds
(without alignments)
324.949 Million cell updates/sec

Title: US-09-843-221A-165
Perfect score: 31
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3709

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : PIR_76:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	%		DB	ID	Description
		Query	Match Length			
1	5	16.1	34	2	A84241	hypothetical prote
2	5	16.1	34	2	B97032	transcription regu
3	5	16.1	35	2	E95098	hypothetical prote
4	4	12.9	28	2	T09594	gene LFY protein -
5	4	12.9	29	1	A55527	pyrroloquinoline q
6	4	12.9	29	2	S01614	dystrophin - rat (
7	4	12.9	29	2	I78537	copper transportin
8	4	12.9	29	2	S78412	ribosomal protein
9	4	12.9	30	2	S63531	hypothetical prote
10	4	12.9	31	2	S44471	glucagon G1 - Nort
11	4	12.9	31	2	S44472	glucagon G2 - Nort
12	4	12.9	31	2	D70236	hypothetical prote
13	4	12.9	32	2	F23454	ovalbumin phosphos

14	4	12.9	32	2	D31461	T-cell receptor de
15	4	12.9	32	2	G84161	hypothetical prote
16	4	12.9	33	2	E81714	hypothetical prote
17	4	12.9	35	2	D23454	ovalbumin phosphos
18	4	12.9	35	2	G23454	ovalbumin phosphos
19	4	12.9	35	2	D82125	hypothetical prote
20	4	12.9	36	2	S70806	hypothetical prote
21	4	12.9	36	2	F95057	hypothetical prote
22	4	12.9	36	2	A84774	hypothetical prote
23	4	12.9	36	2	S46227	hypothetical prote
24	4	12.9	37	2	S71912	hemoglobin, extrac
25	4	12.9	37	2	T12635	homeotic protein H
26	4	12.9	39	1	CKFHCS	sarcotoxin IC - fl
27	4	12.9	39	2	S71913	hemoglobin, extrac
28	4	12.9	39	2	S77164	ycf32 protein - Sy
29	3	9.7	28	2	A42272	brain-type creatin
30	3	9.7	28	2	C32416	phospholipase A2 (
31	3	9.7	28	2	B60071	vasoactive intesti
32	3	9.7	28	2	A60304	vasoactive intesti
33	3	9.7	28	2	S58386	T-cell receptor be
34	3	9.7	28	2	PN0047	signal transductio
35	3	9.7	28	2	S70894	hypothetical prote
36	3	9.7	28	2	S22469	hypothetical prote
37	3	9.7	28	2	S26254	rel protein - chic
38	3	9.7	28	2	I59477	antigen, T-cell re
39	3	9.7	28	2	F46522	T-cell receptor et
40	3	9.7	28	2	H85908	hypothetical prote
41	3	9.7	29	1	GCCB	glucagon - Chinch
42	3	9.7	29	2	S39968	probable hydro-lya
43	3	9.7	29	2	A61509	islet amyloid poly
44	3	9.7	29	2	S17147	galanin - chicken
45	3	9.7	29	2	T44245	ribosomal protein
46	3	9.7	29	2	A05272	gelsolin, cytosoli
47	3	9.7	29	2	B44101	calmodulin, vasoac
48	3	9.7	29	2	S42642	probable rhicadhes
49	3	9.7	29	2	A00774	3-oxoadipate enol-
50	3	9.7	29	2	B81136	hypothetical prote
51	3	9.7	29	2	I84189	cyclic AMP recepto
52	3	9.7	29	2	S65747	CDP-paratose synth
53	3	9.7	29	2	S65748	CDP-paratose synth
54	3	9.7	29	2	B41476	probable antigen 2
55	3	9.7	29	2	S68094	2,3-dihydroxybenzo
56	3	9.7	29	2	A27688	mammary-derived gr
57	3	9.7	29	2	T31443	cytochrome bc chai
58	3	9.7	29	2	F85570	hypothetical prote
59	3	9.7	29	2	I49732	NADH2 dehydrogenas
60	3	9.7	29	2	A59479	NADP phosphatase I
61	3	9.7	30	2	S40309	tyrosine 3-monooxy
62	3	9.7	30	2	C21897	ornithine carbamoy
63	3	9.7	30	2	A28562	glutathione transf
64	3	9.7	30	2	A05315	pancreatic ribonuc
65	3	9.7	30	2	A44598	endo-1,4-beta-xyla
66	3	9.7	30	2	A61333	trypsin (EC 3.4.21
67	3	9.7	30	2	S21815	H+-exporting ATPas
68	3	9.7	30	2	A44912	cysteine proteinas
69	3	9.7	30	2	B61125	glucagon-like pept
70	3	9.7	30	2	C61125	glucagon-like pept

71	3	9.7	30	2	F32502	T-cell receptor de
72	3	9.7	30	2	PD0013	cAMP response elem
73	3	9.7	30	2	S21195	spectrin beta chai
74	3	9.7	30	2	PC4172	profilin - rat (fr
75	3	9.7	30	2	A34461	heat shock protein
76	3	9.7	30	2	A22977	delta-endotoxin -
77	3	9.7	30	2	A44913	34K core flagella
78	3	9.7	30	2	S08565	ribulose-bisphosph
79	3	9.7	30	2	S30333	N-carbamoyl-D-amin
80	3	9.7	30	2	PQ0444	hypothetical prote
81	3	9.7	30	2	H95021	hypothetical prote
82	3	9.7	30	2	D72276	hypothetical prote
83	3	9.7	30	2	D70253	conserved hypothet
84	3	9.7	30	2	B70165	hypothetical prote
85	3	9.7	30	2	B81956	hypothetical prote
86	3	9.7	30	2	E82294	hypothetical prote
87	3	9.7	30	2	S72626	small-cell-variant
88	3	9.7	30	2	A35687	probable 39K inorg
89	3	9.7	30	2	S73316	photosystem I chai
90	3	9.7	30	2	A32946	trypsin-like serin
91	3	9.7	30	2	PL0189	Ig light chain - s
92	3	9.7	30	2	S65519	carcinoembryonic a
93	3	9.7	30	2	S34765	4-hydroxybutyryl-C
94	3	9.7	30	2	D81532	hypothetical prote
95	3	9.7	30	2	A48923	retrovirus-related
96	3	9.7	30	2	B56586	storage hexamer 2
97	3	9.7	30	2	F81360	very hypothetical
98	3	9.7	30	2	S15650	NADH2 dehydrogenas
99	3	9.7	30	2	H97596	hypothetical prote
100	3	9.7	30	4	I52605	hypothetical MLL/E
101	3	9.7	31	1	A28805	leiurotoxin I [val
102	3	9.7	31	1	A49078	leiurotoxin I-like
103	3	9.7	31	1	S34504	photosystem I prot
104	3	9.7	31	2	T44925	hypothetical prote
105	3	9.7	31	2	S39019	glucagon-like pept
106	3	9.7	31	2	A58793	relaxin chain B -
107	3	9.7	31	2	A58586	conotoxin MrVIA -
108	3	9.7	31	2	F30608	Ig kappa chain V-I
109	3	9.7	31	2	D30608	Ig kappa chain V-I
110	3	9.7	31	2	F31461	T-cell receptor de
111	3	9.7	31	2	S03295	Ig alpha chain C r
112	3	9.7	31	2	S03297	Ig alpha chain C r
113	3	9.7	31	2	I52232	tau protein - huma
114	3	9.7	31	2	A36162	neutrophil-activat
115	3	9.7	31	2	S04980	ferritin heavy cha
116	3	9.7	31	2	S32610	antiviral protein
117	3	9.7	31	2	S38881	inner membrane pro
118	3	9.7	31	2	G95018	hypothetical prote
119	3	9.7	31	2	G95022	hypothetical prote
120	3	9.7	31	2	A95085	hypothetical prote
121	3	9.7	31	2	H95093	hypothetical prote
122	3	9.7	31	2	E95140	hypothetical prote
123	3	9.7	31	2	E95151	hypothetical prote
124	3	9.7	31	2	E70202	hypothetical prote
125	3	9.7	31	2	E70223	hypothetical prote
126	3	9.7	31	2	H70225	hypothetical prote
127	3	9.7	31	2	C70240	hypothetical prote

128	3	9.7	31	2	E64562	hypothetical prote
129	3	9.7	31	2	S49191	hypothetical prote
130	3	9.7	31	2	H82353	hypothetical prote
131	3	9.7	31	2	A05051	hypothetical prote
132	3	9.7	31	2	B23605	histone H1.3 - whe
133	3	9.7	31	2	S78738	protein YOL038c-a
134	3	9.7	31	2	A36221	cecropin P1 - pig
135	3	9.7	31	2	S27112	sarcolipin - rabbi
136	3	9.7	31	2	D81591	hypothetical prote
137	3	9.7	31	2	G81558	hypothetical prote
138	3	9.7	31	2	G82816	hypothetical prote
139	3	9.7	31	2	F82565	hypothetical prote
140	3	9.7	32	1	TCEE	calcitonin - Japan
141	3	9.7	32	1	TCON2	calcitonin 2 - soc
142	3	9.7	32	1	TCON2C	calcitonin 2 - chu
143	3	9.7	32	1	TCON2P	calcitonin 2 - pin
144	3	9.7	32	1	TCON3	calcitonin 3 - coh
145	3	9.7	32	2	S20719	alcohol dehydrogen
146	3	9.7	32	2	A61143	trypsin (EC 3.4.21
147	3	9.7	32	2	D32502	T-cell receptor de
148	3	9.7	32	2	A32502	T-cell receptor de
149	3	9.7	32	2	B40186	ubiquitin / riboso
150	3	9.7	32	2	S57780	histone H3 - rice
151	3	9.7	32	2	A24047	gap junction prote
152	3	9.7	32	2	S51524	anchorin CII - bov
153	3	9.7	32	2	S36809	GTP-binding regula
154	3	9.7	32	2	A29743	translation initia
155	3	9.7	32	2	A03367	lectin - Macrotylo
156	3	9.7	32	2	A44900	fimbrin, SEF 21 -
157	3	9.7	32	2	S03273	photosystem II oxy
158	3	9.7	32	2	C46107	polyomavirus enhan
159	3	9.7	32	2	S08482	regulatory protein
160	3	9.7	32	2	E87694	hypothetical prote
161	3	9.7	32	2	D70222	hypothetical prote
162	3	9.7	32	2	E70225	hypothetical prote
163	3	9.7	32	2	B70241	hypothetical prote
164	3	9.7	32	2	B70257	hypothetical prote
165	3	9.7	32	2	D82353	hypothetical prote
166	3	9.7	32	2	E82279	hypothetical prote
167	3	9.7	32	2	E82089	hypothetical prote
168	3	9.7	32	2	H82416	hypothetical prote
169	3	9.7	32	2	T17394	vrlN protein - Dic
170	3	9.7	32	2	S23476	hypothetical prote
171	3	9.7	32	2	S22304	hypothetical prote
172	3	9.7	32	2	S78323	photosystem II pro
173	3	9.7	32	2	A05015	hypothetical prote
174	3	9.7	32	2	I38619	zinc finger protei
175	3	9.7	32	2	S28398	t-complex protein
176	3	9.7	32	2	T14569	hypothetical prote
177	3	9.7	32	2	H84081	hypothetical prote
178	3	9.7	32	2	F82833	hypothetical prote
179	3	9.7	32	2	JC5802	ovulation stimulat
180	3	9.7	32	2	E85588	hypothetical prote
181	3	9.7	33	2	S43312	2',3'-cyclic-nucle
182	3	9.7	33	2	S26859	chitinase (EC 3.2.
183	3	9.7	33	2	I52219	c-ras-Ki-2 protein
184	3	9.7	33	2	I53221	K-ras protein - hu

185	3	9.7	33	2	PC2300	gaegurin 1 - Korea
186	3	9.7	33	2	I56451	relaxin - hamadrya
187	3	9.7	33	2	E32502	T-cell receptor de
188	3	9.7	33	2	A31461	T-cell receptor de
189	3	9.7	33	2	B31461	T-cell receptor de
190	3	9.7	33	2	A03150	retinoic acid-bind
191	3	9.7	33	2	C46027	neurotransmitter t
192	3	9.7	33	2	PQ0150	dnaK-type molecula
193	3	9.7	33	2	B44906	L1 protein - human
194	3	9.7	33	2	PQ0418	matrix protein M1
195	3	9.7	33	2	S34505	hypothetical prote
196	3	9.7	33	2	G95006	hypothetical prote
197	3	9.7	33	2	C95200	hypothetical prote
198	3	9.7	33	2	A87213	hypothetical prote
199	3	9.7	33	2	F84163	hypothetical prote
200	3	9.7	33	2	E82135	hypothetical prote
201	3	9.7	33	2	H82475	hypothetical prote
202	3	9.7	33	2	S68096	lactate dehydrogen
203	3	9.7	33	2	E82526	hypothetical prote
204	3	9.7	33	2	AC1012	hypothetical prote
205	3	9.7	33	2	C97406	hypothetical prote
206	3	9.7	34	2	S57282	phospholipase A2 (
207	3	9.7	34	2	A40298	dermaseptin - Sauv
208	3	9.7	34	2	JS0426	big gastrin - goat
209	3	9.7	34	2	I48887	cryptdin-4 - mouse
210	3	9.7	34	2	I32502	T-cell receptor de
211	3	9.7	34	2	H31461	T-cell receptor de
212	3	9.7	34	2	A19197	class II histocomp
213	3	9.7	34	2	D48147	troponin I (altern
214	3	9.7	34	2	A43564	neurogenic protein
215	3	9.7	34	2	H95047	hypothetical prote
216	3	9.7	34	2	D95189	hypothetical prote
217	3	9.7	34	2	C90973	hypothetical prote
218	3	9.7	34	2	F70242	hypothetical prote
219	3	9.7	34	2	B70252	hypothetical prote
220	3	9.7	34	2	F81919	hypothetical prote
221	3	9.7	34	2	H81883	hypothetical prote
222	3	9.7	34	2	F81044	hypothetical prote
223	3	9.7	34	2	F82163	hypothetical prote
224	3	9.7	34	2	E82100	hypothetical prote
225	3	9.7	34	2	B82449	hypothetical prote
226	3	9.7	34	2	S13662	cellulase (EC 3.2.
227	3	9.7	34	2	A60110	repetitive protein
228	3	9.7	34	2	S44828	F54F2.3 protein -
229	3	9.7	34	2	S40662	P-cadherin - mouse
230	3	9.7	34	2	F84079	hypothetical prote
231	3	9.7	34	2	H81600	hypothetical prote
232	3	9.7	34	2	H82820	hypothetical prote
233	3	9.7	34	2	C82819	hypothetical prote
234	3	9.7	34	2	C82764	hypothetical prote
235	3	9.7	34	2	B82679	hypothetical prote
236	3	9.7	34	2	G85820	unknown protein en
237	3	9.7	34	2	S12554	hydroxymethylgluta
238	3	9.7	35	2	E38601	Ig kappa chain V r
239	3	9.7	35	2	A05302	hemoglobin beta ch
240	3	9.7	35	2	A29663	histone H4 - starf
241	3	9.7	35	2	S27154	ribosomal protein

242	3	9.7	35	2	E48401	ribosomal protein
243	3	9.7	35	2	S13435	lectin III - furze
244	3	9.7	35	2	S74556	photosystem II psb
245	3	9.7	35	2	S18224	filamentous hemagg
246	3	9.7	35	2	S18226	opacity protein op
247	3	9.7	35	2	T07870	major latex protei
248	3	9.7	35	2	B33770	hypothetical prote
249	3	9.7	35	2	PS0439	potassium channel
250	3	9.7	35	2	I48925	homeobox protein -
251	3	9.7	35	2	F87622	hypothetical prote
252	3	9.7	35	2	C96619	protein T30E16.7 [
253	3	9.7	35	2	B84674	hypothetical prote
254	3	9.7	35	2	F84395	hypothetical prote
255	3	9.7	35	2	B82012	hypothetical prote
256	3	9.7	35	2	H81948	hypothetical prote
257	3	9.7	35	2	A82151	hypothetical prote
258	3	9.7	35	2	F82051	hypothetical prote
259	3	9.7	35	2	S58708	neutral phosphatas
260	3	9.7	35	2	F69827	hypothetical prote
261	3	9.7	35	2	C69977	hypothetical prote
262	3	9.7	35	2	S65772	early nodulin 40 -
263	3	9.7	35	2	A38107	mammalian toxin -
264	3	9.7	35	2	S49309	oncofetal protein
265	3	9.7	35	2	C81560	hypothetical prote
266	3	9.7	35	2	B85708	unknown protein en
267	3	9.7	36	2	H32502	T-cell receptor de
268	3	9.7	36	2	C32502	T-cell receptor de
269	3	9.7	36	2	S08552	ribosomal protein
270	3	9.7	36	2	S72299	ribosomal protein
271	3	9.7	36	2	B44400	myosin heavy chain
272	3	9.7	36	2	I46593	myosin - pig (frag
273	3	9.7	36	2	B31872	retinoic acid-bind
274	3	9.7	36	2	S35572	zona pellucida pro
275	3	9.7	36	2	B41481	virulence-associat
276	3	9.7	36	2	A38659	methanol dehydroge
277	3	9.7	36	2	C95218	conserved domain p
278	3	9.7	36	2	E84416	hypothetical prote
279	3	9.7	36	2	S17834	acetyl-CoA carboxy
280	3	9.7	36	2	E70220	hypothetical prote
281	3	9.7	36	2	E70238	hypothetical prote
282	3	9.7	36	2	F64604	hypothetical prote
283	3	9.7	36	2	G81853	hypothetical prote
284	3	9.7	36	2	S16552	hypothetical prote
285	3	9.7	36	2	G82281	hypothetical prote
286	3	9.7	36	2	A82163	hypothetical prote
287	3	9.7	36	2	C82111	hypothetical prote
288	3	9.7	36	2	A82092	hypothetical prote
289	3	9.7	36	2	B82093	hypothetical prote
290	3	9.7	36	2	A82437	hypothetical prote
291	3	9.7	36	2	A38729	pyruvate decarboxy
292	3	9.7	36	2	A69326	hypothetical prote
293	3	9.7	36	2	S67795	probable membrane
294	3	9.7	36	2	T22263	hypothetical prote
295	3	9.7	36	2	A57443	guanylate cyclase
296	3	9.7	36	2	D83682	hypothetical prote
297	3	9.7	36	2	A83870	hypothetical prote
298	3	9.7	36	2	F84074	hypothetical prote

299	3	9.7	36	2	A56634	neuropeptide F - A
300	3	9.7	36	2	S77071	probable plastoqui
301	3	9.7	36	2	AF1015	hypothetical prote
302	3	9.7	36	2	AI1841	hypothetical prote
303	3	9.7	37	1	S32792	iberiotoxin - east
304	3	9.7	37	1	HSWT93	histone H2A.3 - wh
305	3	9.7	37	2	S48656	fusicoccin recepto
306	3	9.7	37	2	S03570	trypsin (EC 3.4.21
307	3	9.7	37	2	S39367	proteinase omega -
308	3	9.7	37	2	S06217	transforming prote
309	3	9.7	37	2	S05037	insulinoma amyloid
310	3	9.7	37	2	A30607	Ig kappa chain V-I
311	3	9.7	37	2	PC1121	antifungal 25K pro
312	3	9.7	37	2	G01887	MEK kinase - human
313	3	9.7	37	2	S07517	gene 6.3 protein -
314	3	9.7	37	2	G70223	hypothetical prote
315	3	9.7	37	2	E70241	hypothetical prote
316	3	9.7	37	2	D83199	hypothetical prote
317	3	9.7	37	2	H82304	hypothetical prote
318	3	9.7	37	2	S21132	photosystem II cyt
319	3	9.7	37	2	F59103	hypothetical prote
320	3	9.7	37	2	T36662	small hypothetical
321	3	9.7	37	2	T11815	hypothetical prote
322	3	9.7	37	2	A57127	diuretic hormone 1
323	3	9.7	37	2	C32112	R15 gamma peptide
324	3	9.7	37	2	B48845	sterol regulatory
325	3	9.7	37	2	S68261	hypothetical prote
326	3	9.7	37	2	S49982	Tcell receptor alp
327	3	9.7	37	2	B39030	androgen-binding p
328	3	9.7	37	2	PN0550	metabotropic gluta
329	3	9.7	37	2	S70931	histone-like prote
330	3	9.7	37	2	F81403	hypothetical prote
331	3	9.7	38	1	R5EC36	ribosomal protein
332	3	9.7	38	2	C34047	stylar glycoprotei
333	3	9.7	38	2	T11763	acetyl-CoA carboxy
334	3	9.7	38	2	S39034	lipid transfer pro
335	3	9.7	38	2	A42974	natriuretic peptid
336	3	9.7	38	2	A49165	pituitary adenylat
337	3	9.7	38	2	A61070	pituitary adenylat
338	3	9.7	38	2	PS0129	H-2 class I histoc
339	3	9.7	38	2	S50764	ribosomal protein
340	3	9.7	38	2	E72247	ribosomal protein
341	3	9.7	38	2	H83113	50S ribosomal prot
342	3	9.7	38	2	AG0028	50S ribosomal prot
343	3	9.7	38	2	D91149	50S ribosomal subu
344	3	9.7	38	2	AF1008	50S ribosomal chai
345	3	9.7	38	2	PH1920	annexin-like 40K p
346	3	9.7	38	2	S72344	pile protein - Nei
347	3	9.7	38	2	A60216	hyperglycemic horm
348	3	9.7	38	2	S65416	pyruvate synthase
349	3	9.7	38	2	B95069	hypothetical prote
350	3	9.7	38	2	A95139	hypothetical prote
351	3	9.7	38	2	H91111	hypothetical prote
352	3	9.7	38	2	D90631	hypothetical prote
353	3	9.7	38	2	E72306	hypothetical prote
354	3	9.7	38	2	E81873	hypothetical prote
355	3	9.7	38	2	T14885	hypothetical prote

356	3	9.7	38	2	A82478	hypothetical prote
357	3	9.7	38	2	E82463	hypothetical prote
358	3	9.7	38	2	A82450	hypothetical prote
359	3	9.7	38	2	D37842	hypothetical prote
360	3	9.7	38	2	B69492	hypothetical prote
361	3	9.7	38	2	S23173	photosystem I chai
362	3	9.7	38	2	T01992	hypothetical prote
363	3	9.7	38	2	S58601	hypothetical prote
364	3	9.7	38	2	T01741	hypothetical prote
365	3	9.7	38	2	B39888	synapsin I - bovin
366	3	9.7	38	2	B49012	orf 5' of meg1 - m
367	3	9.7	38	2	A83863	hypothetical prote
368	3	9.7	38	2	H81603	hypothetical prote
369	3	9.7	38	2	E82858	hypothetical prote
370	3	9.7	38	2	G71305	probable ribosomal
371	3	9.7	38	2	B97327	hypothetical prote
372	3	9.7	38	2	E86077	hypothetical prote
373	3	9.7	38	2	H85994	50S ribosomal subu
374	3	9.7	38	2	T08652	hypothetical prote
375	3	9.7	38	2	AB0747	hypothetical prote
376	3	9.7	38	2	AH0774	hypothetical prote
377	3	9.7	38	2	C97551	hypothetical prote
378	3	9.7	39	1	CTDFAS	corticotropin - sp
379	3	9.7	39	1	HWGH3Z	exendin-3 - Mexica
380	3	9.7	39	1	HWGH4G	exendin-4 - Gila m
381	3	9.7	39	2	B45946	gamma-glutamyltran
382	3	9.7	39	2	I55325	aspartate transami
383	3	9.7	39	2	S09645	hygromycin-B kinas
384	3	9.7	39	2	A01458	corticotropin - fi
385	3	9.7	39	2	PN0127	corticotropin - se
386	3	9.7	39	2	A61127	adrenocorticotropi
387	3	9.7	39	2	A01459	corticotropin - os
388	3	9.7	39	2	A01457	corticotropin - ra
389	3	9.7	39	2	C55995	prostaglandin E2 r
390	3	9.7	39	2	S07458	Ig kappa chain V r
391	3	9.7	39	2	PH0878	Ig kappa chain V r
392	3	9.7	39	2	S72459	ribosomal protein
393	3	9.7	39	2	PQ0011	tubulin beta chain
394	3	9.7	39	2	S63482	tubulin beta chain
395	3	9.7	39	2	A45793	actin - nematode (
396	3	9.7	39	2	AH2286	photosystem II pro
397	3	9.7	39	2	G64944	yebJ protein - Esc
398	3	9.7	39	2	A85795	hypothetical prote
399	3	9.7	39	2	S78008	fucosyltransferase
400	3	9.7	39	2	A48110	RNA recognition mo
401	3	9.7	39	2	H95146	hypothetical prote
402	3	9.7	39	2	D70239	hypothetical prote
403	3	9.7	39	2	C70254	hypothetical prote
404	3	9.7	39	2	G81899	hypothetical prote
405	3	9.7	39	2	B81912	hypothetical prote
406	3	9.7	39	2	B81954	very hypothetical
407	3	9.7	39	2	F82329	hypothetical prote
408	3	9.7	39	2	A43591	43K outer membrane
409	3	9.7	39	2	A44918	lactococcin G pept
410	3	9.7	39	2	S67938	hypothetical prote
411	3	9.7	39	2	S73118	photosystem II pro
412	3	9.7	39	2	PC4294	high mobility grou

413	3	9.7	39	2	T15158	hypothetical prote
414	3	9.7	39	2	I46466	luteinizing hormon
415	3	9.7	39	2	B40984	finger protein zfe
416	3	9.7	39	2	T03365	gene e2 protein -
417	3	9.7	39	2	F81587	hypothetical prote
418	3	9.7	39	2	E81540	hypothetical prote
419	3	9.7	39	2	T12905	hypothetical prote
420	3	9.7	39	2	AD0162	hypothetical prote
421	3	9.7	39	2	AE3109	hypothetical prote
422	3	9.7	40	1	SWFGS	sauvagine - Sauvag
423	3	9.7	40	2	B61320	plastocyanin - Aqu
424	3	9.7	40	2	S52343	hypothetical prote
425	3	9.7	40	2	S00264	creatine kinase (E
426	3	9.7	40	2	S34407	adenylate kinase (
427	3	9.7	40	2	PQ0202	endo-1,4-beta-xyla
428	3	9.7	40	2	S50021	trypsin-like prote
429	3	9.7	40	2	B60908	beta-lactamase (EC
430	3	9.7	40	2	B41440	protein disulfide-
431	3	9.7	40	2	A19940	antithrombin III -
432	3	9.7	40	2	B59005	thymosin beta - sc
433	3	9.7	40	2	A59005	thymosin beta - se
434	3	9.7	40	2	B31791	sarcotoxin ID - fl
435	3	9.7	40	2	S07969	T-cell receptor al
436	3	9.7	40	2	I50012	MHC class I protei
437	3	9.7	40	2	I50013	MHC class I protei
438	3	9.7	40	2	S61539	ribosomal protein
439	3	9.7	40	2	A60171	proteoglycan core
440	3	9.7	40	2	A60645	tubulin beta chain
441	3	9.7	40	2	A29184	vitellogenin - tur
442	3	9.7	40	2	S65907	conglutin gamma -
443	3	9.7	40	2	S08656	protein VI - human
444	3	9.7	40	2	A53708	indolepyruvate syn
445	3	9.7	40	2	T08107	nonenzymatic prote
446	3	9.7	40	2	S71917	hemoglobin, extrac
447	3	9.7	40	2	S58853	homeotic protein u
448	3	9.7	40	2	H95063	hypothetical prote
449	3	9.7	40	2	H91281	hypothetical prote
450	3	9.7	40	2	A87642	hypothetical prote
451	3	9.7	40	2	F87419	hypothetical prote
452	3	9.7	40	2	C32338	hypothetical 4K pr
453	3	9.7	40	2	C72398	hypothetical prote
454	3	9.7	40	2	S44935	hypothetical prote
455	3	9.7	40	2	A82203	hypothetical prote
456	3	9.7	40	2	G82484	hypothetical prote
457	3	9.7	40	2	A82382	hypothetical prote
458	3	9.7	40	2	I39944	regulatory extrace
459	3	9.7	40	2	F69677	phosphatase (RapK)
460	3	9.7	40	2	I41476	probable antigen 9
461	3	9.7	40	2	S27709	hypothetical prote
462	3	9.7	40	2	F45095	photosystem I ligh
463	3	9.7	40	2	T11811	hypothetical prote
464	3	9.7	40	2	T07472	hypothetical prote
465	3	9.7	40	2	T07516	hypothetical prote
466	3	9.7	40	2	T07523	hypothetical prote
467	3	9.7	40	2	T07560	hypothetical prote
468	3	9.7	40	2	T48629	hypothetical prote
469	3	9.7	40	2	S53001	mitotic-specific c

470	3	9.7	40	2	T03831	hypothetical prote
471	3	9.7	40	2	S71295	deoxyguanosine kin
472	3	9.7	40	2	S56768	capsid protein - L
473	3	9.7	40	2	T07206	hypothetical prote
474	3	9.7	40	2	H81592	hypothetical prote
475	3	9.7	40	2	H81520	hypothetical prote
476	3	9.7	40	2	F81511	hypothetical prote
477	3	9.7	40	2	G82620	hypothetical prote
478	3	9.7	40	2	A82590	hypothetical prote
479	3	9.7	40	2	A86123	hypothetical prote
480	3	9.7	40	2	B97413	hypothetical prote
481	2	6.5	28	1	LFSEW	trp operon leader
482	2	6.5	28	1	LFEBLT	leu operon leader
483	2	6.5	28	1	LFECCL	leu operon leader
484	2	6.5	28	1	G9BPSV	gene 9 protein - s
485	2	6.5	28	2	S41774	ubiquinol-cytochro
486	2	6.5	28	2	S71598	cytochrome P450 HP
487	2	6.5	28	2	S04341	cytochrome P450 PB
488	2	6.5	28	2	PX0033	cytochrome P450 te
489	2	6.5	28	2	S66436	allophycocyanin al
490	2	6.5	28	2	S47624	D-aspartate oxidas
491	2	6.5	28	2	T14210	NADH2 dehydrogenas
492	2	6.5	28	2	T14213	NADH2 dehydrogenas
493	2	6.5	28	2	T12301	NADH2 dehydrogenas
494	2	6.5	28	2	PC1162	cytochrome-c oxida
495	2	6.5	28	2	S21278	glutathione transf
496	2	6.5	28	2	C33948	glutathione transf
497	2	6.5	28	2	A34244	hexokinase (EC 2.7
498	2	6.5	28	2	D38578	protein kinase 4 (
499	2	6.5	28	2	B39116	epidermal growth f
500	2	6.5	28	2	A31859	deoxycytidine kina
501	2	6.5	28	2	B54257	deoxynucleoside ki
502	2	6.5	28	2	I55596	lysosomal acid lip
503	2	6.5	28	2	B35948	phospholipase A2 (
504	2	6.5	28	2	C35948	phospholipase A2 (
505	2	6.5	28	2	A35115	hypothetical prote
506	2	6.5	28	2	A61281	lysozyme homolog A
507	2	6.5	28	2	A61529	chymotrypsin (EC 3
508	2	6.5	28	2	A60291	24K proteinase (EC
509	2	6.5	28	2	S08186	proteasome beta ch
510	2	6.5	28	2	S55729	orotidine-5'-monop
511	2	6.5	28	2	I40034	trpE protein - Bac
512	2	6.5	28	2	A32643	deoxyribodipyrimid
513	2	6.5	28	2	S77854	glutamate-tRNA lig
514	2	6.5	28	2	JX0059	serine proteinase
515	2	6.5	28	2	S07156	trypsin inhibitor
516	2	6.5	28	2	JX0058	trypsin inhibitor
517	2	6.5	28	2	B45041	trypsin inhibitor
518	2	6.5	28	2	S20393	trypsin inhibitor
519	2	6.5	28	2	A25802	2S seed storage pr
520	2	6.5	28	2	T47196	RAS protein [impor
521	2	6.5	28	2	A61322	somatostatin-28 -
522	2	6.5	28	2	B60583	glycoprotein hormo
523	2	6.5	28	2	A38232	vasoactive intesti
524	2	6.5	28	2	A60303	vasoactive intesti
525	2	6.5	28	2	JT0412	bombyxin-IV chain
526	2	6.5	28	2	A56366	intestinal trefoil

527	2	6.5	28	2	C44180	alpha-neurotoxin-1
528	2	6.5	28	2	C39327	long neurotoxin -
529	2	6.5	28	2	I32529	Ig lambda chain V
530	2	6.5	28	2	PC1001	Ig light chain V r
531	2	6.5	28	2	B47719	T-cell receptor al
532	2	6.5	28	2	D47719	T-cell receptor al
533	2	6.5	28	2	S58389	T-cell receptor be
534	2	6.5	28	2	PH0250	T-cell receptor Vb
535	2	6.5	28	2	PH0247	T-cell receptor Vb
536	2	6.5	28	2	A49829	T-cell receptor va
537	2	6.5	28	2	D49829	T-cell receptor va
538	2	6.5	28	2	PH1908	T-cell receptor al
539	2	6.5	28	2	D41912	T-cell receptor be
540	2	6.5	28	2	G47719	house-dust-mite-re
541	2	6.5	28	2	E49533	T-cell receptor be
542	2	6.5	28	2	I46921	gene Bota protein
543	2	6.5	28	2	S11618	ribosomal protein
544	2	6.5	28	2	S51060	ribosomal protein
545	2	6.5	28	2	S51067	ribosomal protein
546	2	6.5	28	2	S72460	ribosomal protein
547	2	6.5	28	2	S08569	ribosomal protein
548	2	6.5	28	2	S10052	ribosomal protein
549	2	6.5	28	2	S55442	beta A2 crystallin
550	2	6.5	28	2	A45626	beta 2-tubulin - n
551	2	6.5	28	2	S21231	calcium-binding pr
552	2	6.5	28	2	A23691	apolipoprotein C-I
553	2	6.5	28	2	A05296	fibrinogen alpha c
554	2	6.5	28	2	A61113	cellular retinol-b
555	2	6.5	28	2	B35577	cell adhesion rece
556	2	6.5	28	2	I48349	fibronectin - mous
557	2	6.5	28	2	A61233	retinol-binding pr
558	2	6.5	28	2	I45911	dnaK-type molecula
559	2	6.5	28	2	PQ0263	dnaK-type molecula
560	2	6.5	28	2	A03356	omega-gliadin - ei
561	2	6.5	28	2	A60359	pollen allergen DG
562	2	6.5	28	2	A60752	outer membrane pro
563	2	6.5	28	2	PQ0691	photosystem I 5.6K
564	2	6.5	28	2	G32351	34K class B flagel
565	2	6.5	28	2	S47614	zinc finger protei
566	2	6.5	28	2	S49924	stp protein (Baker
567	2	6.5	28	2	B39227	calcium channel pr
568	2	6.5	28	2	F54346	pyruvate synthase
569	2	6.5	28	2	A36153	major allergen Ole
570	2	6.5	28	2	B54127	dolichyl-diphospho
571	2	6.5	28	2	S56746	alpha-synuclein, N
572	2	6.5	28	2	I48178	orphan receptor -
573	2	6.5	28	2	PC4429	peroxisome prolife
574	2	6.5	28	2	PC4430	peroxisome prolife
575	2	6.5	28	2	S29135	aminopyrine N-deme
576	2	6.5	28	2	S29136	aminopyrine N-deme
577	2	6.5	28	2	PN0625	homeobox JRX prote
578	2	6.5	28	2	B56779	tetM 5'-region lea
579	2	6.5	28	2	JU0297	fruR-shl operon le
580	2	6.5	28	2	G90638	leu operon leader
581	2	6.5	28	2	C90639	fruR leader peptid
582	2	6.5	28	2	B47310	MHVS28AA - murine
583	2	6.5	28	2	E64656	hypothetical prote

584	2	6.5	28	2	B64669	hypothetical prote
585	2	6.5	28	2	S15235	hypothetical prote
586	2	6.5	28	2	C56262	uvrB 3'-region hyp
587	2	6.5	28	2	E81239	hypothetical prote
588	2	6.5	28	2	I60364	phosphorybosylpyro
589	2	6.5	28	2	S56121	type I DNA methylt
590	2	6.5	28	2	B39191	hypothetical prote
591	2	6.5	28	2	T17391	hypothetical prote
592	2	6.5	28	2	A56499	brevicin-27 - Lact
593	2	6.5	28	2	A41476	probable antigen 1
594	2	6.5	28	2	S16228	aryl acylamidase -
595	2	6.5	28	2	T37143	hypothetical prote
596	2	6.5	28	2	PS0106	2-phosphinomethylm
597	2	6.5	28	2	G69384	conserved hypothet
598	2	6.5	28	2	A69259	hypothetical prote
599	2	6.5	28	2	T06925	hypothetical prote
600	2	6.5	28	2	S38524	rRNA N-glycosidase
601	2	6.5	28	2	S21742	3-oxoacyl-[acyl-ca
602	2	6.5	28	2	PQ0800	calmodulin antagon
603	2	6.5	28	2	T06340	ribosomal protein
604	2	6.5	28	2	T07599	hypothetical prote
605	2	6.5	28	2	PH0220	peroxidase (EC 1.1
606	2	6.5	28	2	JQ0272	hypothetical 3K pr
607	2	6.5	28	2	S46250	fatty-acid-binding
608	2	6.5	28	2	A44923	carboxypeptidase 3
609	2	6.5	28	2	S64701	hypothetical prote
610	2	6.5	28	2	T38041	similarity to yeas
611	2	6.5	28	2	A27261	proteinase inhibit
612	2	6.5	28	2	A61417	bdellin B-3 - medi
613	2	6.5	28	2	S06668	toxin-like protein
614	2	6.5	28	2	S07826	venom protein - Am
615	2	6.5	28	2	C34923	omega-agatoxin IIA
616	2	6.5	28	2	A44877	cell surface prote
617	2	6.5	28	2	JW0019	mast cell degranul
618	2	6.5	28	2	A61273	interleukin-1 - st
619	2	6.5	28	2	S68643	nicotinic acetylch
620	2	6.5	28	2	PC2162	angiotensin II rec
621	2	6.5	28	2	I54183	cell adhesion regu
622	2	6.5	28	2	S54338	cytochrome P450 CY
623	2	6.5	28	2	I52627	erythrocyte chemok
624	2	6.5	28	2	JQ1035	hypothetical 3.2K
625	2	6.5	28	2	PH1335	Ig heavy chain DJ
626	2	6.5	28	2	S37683	protein IEF SSP 91
627	2	6.5	28	2	S37686	protein IEF SSP 92
628	2	6.5	28	2	PH1911	T-cell receptor al
629	2	6.5	28	2	I39288	ZF3 domain - human
630	2	6.5	28	2	PL0005	pepsin A (EC 3.4.2
631	2	6.5	28	2	A60692	proline-rich prote
632	2	6.5	28	2	PC2239	heat shock protein
633	2	6.5	28	2	PT0366	T-cell receptor be
634	2	6.5	28	2	I58115	cystic fibrosis tr
635	2	6.5	28	2	A46690	sialic acid-specif
636	2	6.5	28	2	C83797	hypothetical prote
637	2	6.5	28	2	C83969	hypothetical prote
638	2	6.5	28	2	S51593	myrB protein - Mic
639	2	6.5	28	2	C85490	fruR leader peptid
640	2	6.5	28	2	C97078	hypothetical prote

641	2	6.5	28	2	F97000	hypothetical prote
642	2	6.5	28	2	G85489	leu operon leader
643	2	6.5	28	2	AB1093	hypothetical prote
644	2	6.5	28	2	T06490	probable ribulose-
645	2	6.5	28	2	S73563	H ⁺ -transporting tw
646	2	6.5	28	2	AG0516	leu operon leader
647	2	6.5	28	4	I68614	frame shifted FMR1
648	2	6.5	28	4	JN0014	GABA(A) receptor a
649	2	6.5	29	1	TIPU	trypsin inhibitor
650	2	6.5	29	1	TIPU3	trypsin inhibitor
651	2	6.5	29	1	TIPU2B	trypsin inhibitor
652	2	6.5	29	1	GCOPV	glucagon - North A
653	2	6.5	29	1	GCDK	glucagon - duck
654	2	6.5	29	1	A61583	glucagon - ostrich
655	2	6.5	29	1	GCFLE	glucagon - Europea
656	2	6.5	29	1	GCDF	glucagon - smaller
657	2	6.5	29	1	GCEN	glucagon - elephan
658	2	6.5	29	1	GCTTS	glucagon - slider
659	2	6.5	29	1	TNLJBR	trans-activating t
660	2	6.5	29	1	Q1BP57	gene 1.5 protein -
661	2	6.5	29	2	A60558	cytochrome P450 HL
662	2	6.5	29	2	T17079	NADH2 dehydrogenas
663	2	6.5	29	2	T17076	NADH2 dehydrogenas
664	2	6.5	29	2	A48427	flavohemoglobin hm
665	2	6.5	29	2	A54234	cytochrome-c oxida
666	2	6.5	29	2	S08201	peroxidase (EC 1.1
667	2	6.5	29	2	A26208	acetyl-CoA C-acety
668	2	6.5	29	2	A22018	phosphotransferase
669	2	6.5	29	2	S46211	kallikrein rK8 (pK
670	2	6.5	29	2	S28174	heat-shock protein
671	2	6.5	29	2	A32414	bothrolysin (EC 3.
672	2	6.5	29	2	S17432	H ⁺ -transporting tw
673	2	6.5	29	2	S02578	H ⁺ -transporting tw
674	2	6.5	29	2	S23122	peptidylprolyl iso
675	2	6.5	29	2	JU0211	squash-type trypsi
676	2	6.5	29	2	T03653	phospholipid trans
677	2	6.5	29	2	C24536	alpha-amylase/tryp
678	2	6.5	29	2	C25310	alpha-amylase/tryp
679	2	6.5	29	2	D55998	brevinin-2Ed - edi
680	2	6.5	29	2	D53578	brevinin-2Ee - edi
681	2	6.5	29	2	A91740	glucagon - turkey
682	2	6.5	29	2	A91741	glucagon - rabbit
683	2	6.5	29	2	A91742	glucagon - Arabian
684	2	6.5	29	2	S07211	glucagon - marbled
685	2	6.5	29	2	A61135	glucagon - bigeye
686	2	6.5	29	2	C39258	glucagon - common
687	2	6.5	29	2	C60840	glucagon I - Europ
688	2	6.5	29	2	S39018	glucagon - bowfin
689	2	6.5	29	2	A39462	cholestokinin - do
690	2	6.5	29	2	A60791	toxin II.9 - scorp
691	2	6.5	29	2	JH0699	omega-conotoxin MV
692	2	6.5	29	2	A58537	omega-conotoxin MV
693	2	6.5	29	2	I52628	low affinity nerve
694	2	6.5	29	2	C61233	conceptus protein
695	2	6.5	29	2	S10061	Ig heavy chain (cl
696	2	6.5	29	2	PH1328	Ig heavy chain DJ
697	2	6.5	29	2	PH0239	T-cell receptor Vb

698	2	6.5	29	2	PH0251	T-cell receptor Vb
699	2	6.5	29	2	PH0254	T-cell receptor Vb
700	2	6.5	29	2	PH0233	T-cell receptor Vb
701	2	6.5	29	2	E31485	Ig heavy chain V r
702	2	6.5	29	2	H31485	Ig kappa chain V r
703	2	6.5	29	2	G31461	T-cell receptor de
704	2	6.5	29	2	C47719	T-cell receptor al
705	2	6.5	29	2	E47719	house-dust-mite-re
706	2	6.5	29	2	PS0134	H-2 class I histoc
707	2	6.5	29	2	PS0132	H-2 class I histoc
708	2	6.5	29	2	I37534	gene HLA-DRB prote
709	2	6.5	29	2	I37535	gene HLA-DRB prote
710	2	6.5	29	2	I37536	MHC class II histo
711	2	6.5	29	2	I37301	MHC class II histo
712	2	6.5	29	2	I37303	HLA-DR beta - huma
713	2	6.5	29	2	I37306	HLA-DR beta - huma
714	2	6.5	29	2	I50214	protein-tyrosine-p
715	2	6.5	29	2	S07771	histone H2B.2, spe
716	2	6.5	29	2	T04412	histone H3 - barle
717	2	6.5	29	2	S51070	ribosomal protein
718	2	6.5	29	2	S08555	ribosomal protein
719	2	6.5	29	2	PC4231	ribosomal protein
720	2	6.5	29	2	S10050	ribosomal protein
721	2	6.5	29	2	S10049	ribosomal protein
722	2	6.5	29	2	S26229	ribosomal protein
723	2	6.5	29	2	A27561	Meth A tumor-speci
724	2	6.5	29	2	S10725	calmodulin-binding
725	2	6.5	29	2	E33208	calreticulin, uter
726	2	6.5	29	2	C33208	calreticulin, slow
727	2	6.5	29	2	D33208	calreticulin, brai
728	2	6.5	29	2	A45474	thrombospondin 2 -
729	2	6.5	29	2	G39690	neural cell adhesi
730	2	6.5	29	2	A61166	endometrial proges
731	2	6.5	29	2	I52402	alpha-fetoprotein
732	2	6.5	29	2	S57232	homeotic protein s
733	2	6.5	29	2	S06854	chorion class B pr
734	2	6.5	29	2	A43038	auxin-binding prot
735	2	6.5	29	2	T12082	proline-rich prote
736	2	6.5	29	2	S70328	gamma35 secalin -
737	2	6.5	29	2	S29208	avenin gamma-3 - o
738	2	6.5	29	2	S07055	photosystem I prot
739	2	6.5	29	2	S05032	photosystem II pro
740	2	6.5	29	2	S08088	gene VII protein -
741	2	6.5	29	2	F42075	finger protein (cl
742	2	6.5	29	2	T51116	probable precorrin
743	2	6.5	29	2	A53145	high conductance c
744	2	6.5	29	2	A35121	hypothetical prote
745	2	6.5	29	2	S03277	photosystem II 5K
746	2	6.5	29	2	A55891	delta-conotoxin Gm
747	2	6.5	29	2	S32730	homeotic protein -
748	2	6.5	29	2	S57225	labial protein (cl
749	2	6.5	29	2	S32732	homeotic protein -
750	2	6.5	29	2	S32734	homeotic protein -
751	2	6.5	29	2	S32733	homeotic protein -
752	2	6.5	29	2	G90719	hypothetical prote
753	2	6.5	29	2	S07513	gene 5.1 protein -
754	2	6.5	29	2	S14040	hypothetical prote

755	2	6.5	29	2	E64586	hypothetical prote
756	2	6.5	29	2	B64607	hypothetical prote
757	2	6.5	29	2	G64674	hypothetical prote
758	2	6.5	29	2	G83440	KdpF protein PA163
759	2	6.5	29	2	A49288	alcohol dehydrogen
760	2	6.5	29	2	A81078	hypothetical prote
761	2	6.5	29	2	B81006	hypothetical prote
762	2	6.5	29	2	T48910	KdpF protein [vali
763	2	6.5	29	2	A35445	repY protein - Esc
764	2	6.5	29	2	S19943	aadB protein - Kle
765	2	6.5	29	2	A49914	S-layer protein va
766	2	6.5	29	2	E64036	hypothetical prote
767	2	6.5	29	2	B48363	2-hydroxyglutaryl-
768	2	6.5	29	2	C40638	orf 3' of cycI - R
769	2	6.5	29	2	B56817	photosystem I chai
770	2	6.5	29	2	S74572	hypothetical prote
771	2	6.5	29	2	C60743	putrescine carbamo
772	2	6.5	29	2	S67989	HA-19/HA-52 protei
773	2	6.5	29	2	S14099	12-alpha-hydroxyst
774	2	6.5	29	2	S77569	plantaricin SA6 -
775	2	6.5	29	2	S21222	48K protein - Euba
776	2	6.5	29	2	S03947	hydrogen dehydroge
777	2	6.5	29	2	T34643	hypothetical prote
778	2	6.5	29	2	T37120	hypothetical prote
779	2	6.5	29	2	T36654	probable small mem
780	2	6.5	29	2	B43937	endo-1,4-beta-xyla
781	2	6.5	29	2	S09556	hypothetical prote
782	2	6.5	29	2	T06904	hypothetical prote
783	2	6.5	29	2	S73197	hypothetical prote
784	2	6.5	29	2	S78326	conserved hypothet
785	2	6.5	29	2	S78310	hypothetical prote
786	2	6.5	29	2	S78360	hypothetical prote
787	2	6.5	29	2	S01572	hypothetical prote
788	2	6.5	29	2	T07450	hypothetical prote
789	2	6.5	29	2	S01448	hypothetical prote
790	2	6.5	29	2	S38525	rRNA N-glycosidase
791	2	6.5	29	2	T52557	translation elonga
792	2	6.5	29	2	PQ0862	allantoinase (EC 3
793	2	6.5	29	2	PQ0486	globulin 2a - taro
794	2	6.5	29	2	S02200	prolamin alpha-1 -
795	2	6.5	29	2	A60683	malate dehydrogena
796	2	6.5	29	2	JQ0212	hypothetical 3K pr
797	2	6.5	29	2	S58541	hypothetical prote
798	2	6.5	29	2	PC2035	alanine transamina
799	2	6.5	29	2	S78714	protein YDR524w-a
800	2	6.5	29	2	B21112	variant surface gl
801	2	6.5	29	2	C60110	repetitive protein
802	2	6.5	29	2	D24802	cuticle protein 36
803	2	6.5	29	2	A56591	E75 steroid recept
804	2	6.5	29	2	A61613	ceratotoxin A - Me
805	2	6.5	29	2	B61613	ceratotoxin B - Me
806	2	6.5	29	2	PH1230	lectin - namazu (f
807	2	6.5	29	2	A32860	biotin-binding pro
808	2	6.5	29	2	I50382	c-mil protein - ch
809	2	6.5	29	2	I50695	non-collagenous al
810	2	6.5	29	2	B54197	70k thyroid autoan
811	2	6.5	29	2	A35891	carcinoembryonic a

812	2	6.5	29	2	I77372	CD44SP - human
813	2	6.5	29	2	S54340	diazepam binding i
814	2	6.5	29	2	A41683	hyaluronate recept
815	2	6.5	29	2	C54037	splicing regulator
816	2	6.5	29	2	S35924	T-cell receptor ga
817	2	6.5	29	2	C61384	trachael mucin gly
818	2	6.5	29	2	A60604	glutathione peroxi
819	2	6.5	29	2	S57204	oviduct-specific s
820	2	6.5	29	2	I47025	antigen WC1 [impor
821	2	6.5	29	2	A49410	t-complex polypept
822	2	6.5	29	2	PS0125	H-2 class I histoc
823	2	6.5	29	2	S46929	teg169 protein - m
824	2	6.5	29	2	S38749	vimentin homolog -
825	2	6.5	29	2	S42764	Ca2+/calmodulin-de
826	2	6.5	29	2	A49708	synaptosomal-assoc
827	2	6.5	29	2	H83777	hypothetical prote
828	2	6.5	29	2	C83833	hypothetical prote
829	2	6.5	29	2	F83870	hypothetical prote
830	2	6.5	29	2	B84144	hypothetical prote
831	2	6.5	29	2	PC4421	multactivase (EC 3
832	2	6.5	29	2	B85840	hypothetical prote
833	2	6.5	29	2	C85840	hypothetical prote
834	2	6.5	29	2	G86058	hypothetical prote
835	2	6.5	29	2	E89904	hypothetical prote
836	2	6.5	29	2	H89949	hypothetical prote
837	2	6.5	29	2	A59278	neurotoxin BmK A3-
838	2	6.5	29	2	S17496	inorganic diphosph
839	2	6.5	29	2	PQ0782	NADH2 dehydrogenas
840	2	6.5	29	2	S34762	L-serine ammonia-l
841	2	6.5	29	2	AB0717	hypothetical prote
842	2	6.5	29	2	AC0717	hypothetical prote
843	2	6.5	29	2	AH2338	PetN protein [impo
844	2	6.5	29	4	I58970	hypothetical prote
845	2	6.5	30	1	AIBSAF	thermophilic amino
846	2	6.5	30	1	TIPU1W	trypsin inhibitor
847	2	6.5	30	1	OEON2K	beta-endorphin II
848	2	6.5	30	1	IRTRC3	protamine CIII, ma
849	2	6.5	30	1	IRTRC2	protamine Ia - rai
850	2	6.5	30	1	IRTR78	protamine CIII, mi
851	2	6.5	30	1	IRTR4	protamine pTP4 - r
852	2	6.5	30	1	CLHRY2	protamine YII - Pa
853	2	6.5	30	1	CLHR2A	protamine YII - At
854	2	6.5	30	1	SNUMP	sillucin - Rhizomu
855	2	6.5	30	2	I57689	ubiquinol-cytochro
856	2	6.5	30	2	I52254	gene CYP11B2 prote
857	2	6.5	30	2	B56859	fatty acid omega-h
858	2	6.5	30	2	A27375	photosystem I iron
859	2	6.5	30	2	S11131	NADH2 dehydrogenas
860	2	6.5	30	2	S14214	NADH2 dehydrogenas
861	2	6.5	30	2	S08202	peroxidase (EC 1.1
862	2	6.5	30	2	S08204	peroxidase (EC 1.1
863	2	6.5	30	2	S08203	peroxidase (EC 1.1
864	2	6.5	30	2	A39089	hydrogenase (EC 1.
865	2	6.5	30	2	I38066	nitric-oxide synth
866	2	6.5	30	2	I39799	CAT-66 - Bacillus
867	2	6.5	30	2	A18780	dimethylallyltrans
868	2	6.5	30	2	S03283	methionine adenosy

869	2	6.5	30	2	S71865	glutathione transf
870	2	6.5	30	2	B27103	aspartate transami
871	2	6.5	30	2	A27103	aspartate transami
872	2	6.5	30	2	I55427	aspartate transami
873	2	6.5	30	2	A49955	protein-tyrosine k
874	2	6.5	30	2	S68639	nigroxin A - black
875	2	6.5	30	2	S68640	nigroxin B - black
876	2	6.5	30	2	A05004	pancreatic ribonuc
877	2	6.5	30	2	D57001	endo-1,4-beta-xyla
878	2	6.5	30	2	A43937	endo-1,4-beta-xyla
879	2	6.5	30	2	PC2361	alpha-glucosidase
880	2	6.5	30	2	PX0073	epoxide hydrolase
881	2	6.5	30	2	B60291	30K serine protein
882	2	6.5	30	2	A27634	major fecal allerg
883	2	6.5	30	2	B27634	major fecal allerg
884	2	6.5	30	2	I77411	renin-2 - mouse (f
885	2	6.5	30	2	PC2328	proteasome endopep
886	2	6.5	30	2	A34486	inorganic diphosph
887	2	6.5	30	2	S21816	H+-exporting ATPas
888	2	6.5	30	2	S21814	H+-exporting ATPas
889	2	6.5	30	2	S74121	fructose-bisphosph
890	2	6.5	30	2	S25666	phosphopyruvate hy
891	2	6.5	30	2	S69600	peptidylprolyl iso
892	2	6.5	30	2	A60517	alpha-1-antitrypsi
893	2	6.5	30	2	S24979	proteinase inhibit
894	2	6.5	30	2	JX0057	trypsin inhibitor
895	2	6.5	30	2	JS0579	squash-type trypsi
896	2	6.5	30	2	JQ1958	trypsin inhibitor
897	2	6.5	30	2	PC1113	proteinase inhibit
898	2	6.5	30	2	C42842	antifungal 2S stor
899	2	6.5	30	2	S70341	napin large chain
900	2	6.5	30	2	S70343	napin large chain
901	2	6.5	30	2	A33308	thrombomodulin - r
902	2	6.5	30	2	S01657	atrial natriuretic
903	2	6.5	30	2	A61130	somatotropin - Ame
904	2	6.5	30	2	S44473	glucagon-like pept
905	2	6.5	30	2	A59076	defensin alpha-1 -
906	2	6.5	30	2	B59076	defensin alpha-2 -
907	2	6.5	30	2	C59076	defensin alpha-3 -
908	2	6.5	30	2	B60791	toxin II.6 - scorp
909	2	6.5	30	2	A31187	neurotoxin II.22.5
910	2	6.5	30	2	I68109	interferon alpha-W
911	2	6.5	30	2	C49533	T-cell receptor al
912	2	6.5	30	2	S20778	Ig heavy chain V r
913	2	6.5	30	2	PL0092	Ig heavy chain V r
914	2	6.5	30	2	PH0245	T-cell receptor Vb
915	2	6.5	30	2	PH0228	T-cell receptor Vb
916	2	6.5	30	2	PH0252	T-cell receptor Vb
917	2	6.5	30	2	PH0882	Ig kappa chain V r
918	2	6.5	30	2	E31461	T-cell receptor de
919	2	6.5	30	2	PH0235	T-cell receptor Vb
920	2	6.5	30	2	A49533	T-cell receptor al
921	2	6.5	30	2	C27579	T-cell receptor be
922	2	6.5	30	2	I37626	Fc gamma (IgG) rec
923	2	6.5	30	2	PS0121	H-2 class I histoc
924	2	6.5	30	2	S74192	crotoxin inhibitor
925	2	6.5	30	2	A05253	hemoglobin epsilon

926	2	6.5	30	2	A21680	hemoglobin epsilon
927	2	6.5	30	2	A05254	hemoglobin epsilon
928	2	6.5	30	2	S68618	histone H2B - sea
929	2	6.5	30	2	PD0014	cAMP response elem
930	2	6.5	30	2	PN0651	restriction endonu
931	2	6.5	30	2	S11613	ribosomal protein
932	2	6.5	30	2	S11617	ribosomal protein
933	2	6.5	30	2	A60511	gamma-crystallin -
934	2	6.5	30	2	I49412	gamma-crystallin-3
935	2	6.5	30	2	S12965	gamma-crystallin -
936	2	6.5	30	2	S69269	ezrin homolog - bo
937	2	6.5	30	2	A61189	tubulin beta chain
938	2	6.5	30	2	I52806	Duchenne muscular
939	2	6.5	30	2	S21153	calcium-binding pr
940	2	6.5	30	2	A26188	lipocortin I - pig
941	2	6.5	30	2	A56790	annexin, isoform P
942	2	6.5	30	2	A34622	fibrinogen beta ch
943	2	6.5	30	2	A03148	retinol-binding pr
944	2	6.5	30	2	A48299	taurine transporte
945	2	6.5	30	2	B61511	serum albumin, mil
946	2	6.5	30	2	B39819	neutrophil chemota
947	2	6.5	30	2	A38933	vitronectin - bovi
948	2	6.5	30	2	S57234	fushi tarazu segme
949	2	6.5	30	2	S69124	rRNA N-glycosidase
950	2	6.5	30	2	S69125	rRNA N-glycosidase
951	2	6.5	30	2	S07065	rRNA N-glycosidase
952	2	6.5	30	2	A31836	17K antigen - Rick
953	2	6.5	30	2	PQ0669	photosystem I 17.5
954	2	6.5	30	2	E45095	photosystem I ligh
955	2	6.5	30	2	B45095	photosystem I ligh
956	2	6.5	30	2	B24987	regulatory protein
957	2	6.5	30	2	S30757	genome polyprotein
958	2	6.5	30	2	S30760	genome polyprotein
959	2	6.5	30	2	S30759	genome polyprotein
960	2	6.5	30	2	B44314	intracisternal A p
961	2	6.5	30	2	S26175	tail tubular prote
962	2	6.5	30	2	S69352	N-methylhydantoin
963	2	6.5	30	2	S68312	glucuronosyltransf
964	2	6.5	30	2	PH1228	D-aminoacylase (EC
965	2	6.5	30	2	S42364	aromatic-amino-aci
966	2	6.5	30	2	S05223	photosystem I 6.5K
967	2	6.5	30	2	S28991	antifungal protein
968	2	6.5	30	2	PC2307	X-Pro aminopeptida
969	2	6.5	30	2	PQ0484	globulin 1b - taro
970	2	6.5	30	2	C43591	51K outer membrane
971	2	6.5	30	2	B43591	45K outer membrane
972	2	6.5	30	2	S06411	killer plasmid 28K
973	2	6.5	30	2	B49292	GDP dissociation i
974	2	6.5	30	2	A60914	pheromone-binding
975	2	6.5	30	2	PS0437	potassium channel
976	2	6.5	30	2	PS0438	potassium channel
977	2	6.5	30	2	A47607	immunogenic protei
978	2	6.5	30	2	S02088	blood group Rh-rel
979	2	6.5	30	2	S29138	aniline monooxygen
980	2	6.5	30	2	S57227	proboscipedia prot
981	2	6.5	30	2	H95008	hypothetical prote
982	2	6.5	30	2	B95020	hypothetical prote

983	2	6.5	30	2	C95030	hypothetical prote
984	2	6.5	30	2	G95031	hypothetical prote
985	2	6.5	30	2	E95079	hypothetical prote
986	2	6.5	30	2	F95118	hypothetical prote
987	2	6.5	30	2	E95145	hypothetical prote
988	2	6.5	30	2	F89406	protein R10E8.7 [i
989	2	6.5	30	2	F87254	hypothetical prote
990	2	6.5	30	2	E84786	hypothetical prote
991	2	6.5	30	2	C84481	hypothetical prote
992	2	6.5	30	2	B47483	cysteine-rich para
993	2	6.5	30	2	S15141	hypothetical prote
994	2	6.5	30	2	S13985	hypothetical prote
995	2	6.5	30	2	S14038	hypothetical prote
996	2	6.5	30	2	S13994	hypothetical prote
997	2	6.5	30	2	A72205	hypothetical prote
998	2	6.5	30	2	E72356	hypothetical prote
999	2	6.5	30	2	H72312	hypothetical prote
1000	2	6.5	30	2	S66448	trimethylamine deh

ALIGNMENTS

RESULT 1

A84241

hypothetical protein Vng0840h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84241

R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.; Hall, J.; Dahl, T.A.; Welti, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.; Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich, J.L.; Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000

A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe, T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.

A;Title: Genome sequence of Halobacterium species NRC-1.

A;Reference number: A84160; MUID:20504483; PMID:11016950

A;Accession: A84241

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <STO>

A;Cross-references: GB:AE004437; NID:g10580410; PIDN:AAG19293.1; GSPDB:GN00138

C;Genetics:

A;Gene: VNG0840H

Query Match 16.1%; Score 5; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 93;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28

|||||

Db 26 LRKKL 30

RESULT 2

B97032

transcription regulator, AcrR family [imported] - *Clostridium acetobutylicum*

C;Species: *Clostridium acetobutylicum*

C;Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C;Accession: B97032

R;Nolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, H.M.; Dubois, J.; Qiu, D.; Hitti, J.; Wolf, Y.I.; Tatusov, R.L.; Sabathe, F.; Doucette-Stamm, L.; Soucaille, P.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.

J. Bacteriol. 183, 4823-4838, 2001

A;Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*.

A;Reference number: A96900; MUID:21359325; PMID:21359325

A;Accession: B97032

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-34 <KUR>

A;Cross-references: GB:AE001437; PIDN:AAK79045.1; PID:g15023984; GSPDB:GN00168

A;Experimental source: *Clostridium acetobutylicum* ATCC824

C;Genetics:

A;Gene: CAC1071

Query Match 16.1%; Score 5; DB 2; Length 34;

Best Local Similarity 100.0%; Pred. No. 93;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5

||||

Db 30 SVSEI 34

RESULT 3

E95098

hypothetical protein SP0853 [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C;Species: *Streptococcus pneumoniae*

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: E95098

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: E95098

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-35 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74982.1; PID:g14972326; GSPDB:GN00164; TIGR:SP4SP0853

A;Experimental source: strain TIGR4

C;Genetics:
A;Gene: SP0853

Query Match 16.1%; Score 5; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||||
Db 30 KKLQD 34

RESULT 4

T09594

gene LFY protein - Monterey pine (fragment)

C;Species: Pinus radiata (Monterey pine)

C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C;Accession: T09594

R;Izquierdo, L.Y.; Vergara, R.F.; Alvarez-Buylla, E.R.

submitted to the EMBL Data Library, August 1996

A;Description: Partial characterization of Pinus radiata meristem identity homolog gene (LFY).

A;Reference number: Z16756

A;Accession: T09594

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <IZQ>

A;Cross-references: EMBL:U66725; NID:g1513305; PID:g1513306

C;Genetics:

A;Gene: LFY

C;Function:

A;Description: controls meristem identity

Query Match 12.9%; Score 4; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 9.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||||
Db 15 LRKK 18

RESULT 5

A55527

pyrroloquinoline quinone precursor pqqD - Methylobacterium extorquens

C;Species: Methylobacterium extorquens

C;Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 18-Feb-2000

C;Accession: A55527

R;Morris, C.J.; Biville, F.; Turlin, E.; Lee, E.; Ellermann, K.; Fan, W.H.;
Ramamoorthi, R.; Springer, A.L.; Lidstrom, M.E.
J. Bacteriol. 176, 1746-1755, 1994

A;Title: Isolation, phenotypic characterization, and complementation analysis of mutants of Methylobacterium extorquens AM1 unable to synthesize pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.

A;Reference number: A55527; MUID:94179111; PMID:8132470

A;Accession: A55527

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-29 <MOR>
A;Cross-references: GB:L25889; NID:g414589; PIDN:AAA17878.1; PID:g414590
C;Genetics:
A;Gene: pqqD
C;Superfamily: pyrroloquinoline quinone precursor pqqA
C;Keywords: quinoprotein
F;16,20/Product: pyrroloquinoline quinone #status predicted <MAT>
F;16-20/Cross-link: pyrroloquinoline quinone (Glu, Tyr) #status predicted

Query Match 12.9%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 8 VSEI 11

RESULT 6

S01614
dystrophin - rat (fragment)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 20-Jun-2000
C;Accession: S01614
R;Nudel, U.; Robzyk, K.; Yaffe, D.
Nature 331, 635-638, 1988
A;Title: Expression of the putative Duchenne muscular dystrophy gene in differentiated myogenic cell cultures and in the brain.
A;Reference number: S01614; MUID:88122671; PMID:3340214
A;Accession: S01614
A;Status: translation not shown
A;Molecule type: DNA
A;Residues: 1-29 <NUD>
A;Cross-references: EMBL:X07000; NID:g56137; PIDN:CAA30057.1; PID:g1334214
C;Genetics:
A;Map position: X
C;Superfamily: dystrophin; alpha-actinin actin-binding domain homology; spectrin/dystrophin repeat homology; WW repeat homology
C;Keywords: actin binding; cytoskeleton

Query Match 12.9%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 7

I78537
copper transporting P-type ATPase - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 21-Jul-2000
C;Accession: I78537
R;Thomas, G.R.; Forbes, J.R.; Roberts, E.A.; Walshe, J.M.; Cox, D.W.

Nature Genet. 9, 210-217, 1995

A;Title: The Wilson disease gene: spectrum of mutations and their consequences.

A;Reference number: I58128; MUID:95235569; PMID:7626145

A;Accession: I78537

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-29 <RES>

A;Cross-references: GB:S77450; NID:g957354; PIDN:AAB34087.1; PID:g957355

C;Genetics:

A;Gene: GDB:ATP7B

A;Cross-references: GDB:120494; OMIM:277900

A;Map position: 13q14.3-13q21.1

Query Match 12.9%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEIQ 6
|||
Db 14 SEIQ 17

RESULT 8

S78412

ribosomal protein RL22/RL24, mitochondrial [validated] - rat (tentative sequence) (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 25-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 21-Jul-2000

C;Accession: S78412; S78413

R;Goldschmidt-Reisin, S.; Graack, H.R.

submitted to the Protein Sequence Database, February 1998

A;Reference number: S78411

A;Accession: S78412

A;Molecule type: protein

A;Residues: 1-29 <GOL>

A;Note: the protein is designated as mitochondrial ribosomal protein L22

A;Accession: S78413

A;Molecule type: protein

A;Residues: 1-10, 'XXP', 14-15, 'X', 17-24 <GO2>

A;Note: the protein is designated as mitochondrial ribosomal protein L24

C;Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 12.9%; Score 4; DB 2; Length 29;
Best Local Similarity 100.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 4 LRKK 7

RESULT 9

S63531

hypothetical protein 1 - Sulfolobus solfataricus (fragment)

C;Species: Sulfolobus solfataricus

C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C;Accession: S63531

R;Jones, C.E.; Fleming, T.M.; Cowan, D.A.; Littlechild, J.A.; Piper, P.W.
Eur. J. Biochem. 233, 800-808, 1995
A;Title: The phosphoglycerate kinase and glyceraldehyde-3-phosphate
dehydrogenase genes from the thermophilic archaeon *Sulfolobus solfataricus*
overlap by 8-bp: isolation, sequencing of the genes and expression in
Escherichia coli.
A;Reference number: S63528; MUID:96085144; PMID:8521845
A;Accession: S63531
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-30 <JON>
A;Cross-references: EMBL:X80178

Query Match 12.9%; Score 4; DB 2; Length 30;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 11 WLRK 14

RESULT 10

S44471
glucagon G1 - North American paddlefish (*Polyodon spathula*)
C;Species: *Polyodon spathula*
C;Date: 18-Sep-1997 #sequence_revision 18-Sep-1997 #text_change 07-May-1999
C;Accession: S44471
R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.
Biochem. J. 300, 339-345, 1994
A;Title: Characterization of insulins and proglucagon-derived peptides from a
phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).
A;Reference number: S44467; MUID:94271144; PMID:8002937
A;Accession: S44471
A;Molecule type: protein
A;Residues: 1-31 <NGU>
A;Experimental source: pancreas
C;Superfamily: glucagon
C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas
F;1-31/Product: glucagon G1 #status predicted <MAT>

Query Match 12.9%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
|||
Db 23 VEWL 26

RESULT 11

S44472
glucagon G2 - North American paddlefish (*Polyodon spathula*)
C;Species: *Polyodon spathula*
C;Date: 19-Mar-1997 #sequence_revision 12-Dec-1997 #text_change 07-May-1999
C;Accession: S44472
R;Nguyen, T.M.; Mommsen, T.P.; Mims, S.M.; Conlon, J.M.

Biochem. J. 300, 339-345, 1994

A;Title: Characterization of insulins and proglucagon-derived peptides from a phylogenetically ancient fish, the paddlefish (*Polyodon spathula*).

A;Reference number: S44467; MUID:94271144; PMID:8002937

A;Accession: S44472

A;Molecule type: protein

A;Residues: 1-31 <NGU>

A;Note: the sequence from Fig. 3 is inconsistent with that from Fig. 5 in having 29-Glu

C;Superfamily: glucagon

C;Keywords: carbohydrate metabolism; duplication; hormone; pancreas

F;1-31/Product: glucagon G2 #status predicted <GCN>

Query Match 12.9%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 21 VEWL 24
 ||||
Db 23 VEWL 26

RESULT 12

D70236

hypothetical protein BBH11 - Lyme disease spirochete plasmid H/lp28-3

C;Species: *Borrelia burgdorferi* (Lyme disease spirochete)

C;Date: 13-Feb-1998 #sequence_revision 13-Feb-1998 #text_change 08-Oct-1999

C;Accession: D70236

R;Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; White, O.; Ketchum, K.A.; Dodson, R.; Hickey, E.K.; Gwinn, M.; Dougherty, B.; Tomb, J.F.; Fleischmann, R.D.; Richardson, D.; Peterson, J.; Kerlavage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vugt, R.V.; Palmer, N.; Adams, M.D.; Gocayne, J.; Weidman, J.; Utterback, T.; Wathney, L.; McDonald, L.; Artiach, P.; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.

Nature 390, 580-586, 1997

A;Authors: Smith, H.O.; Venter, J.C.

A;Title: Genomic sequence of a Lyme disease spirochaete, *Borrelia burgdorferi*.

A;Reference number: A70100; MUID:98065943; PMID:9403685

A;Accession: D70236

A;Status: preliminary; nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-31 <KLE>

A;Cross-references: GB:AE000784; NID:g2690041; PIDN:AAC66002.1; PID:g2690058; TIGR:BBH11

A;Experimental source: strain B31

C;Genetics:

A;Genome: plasmid

Query Match 12.9%; Score 4; DB 2; Length 31;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
Db 26 KKLQ 29

RESULT 13

F23454

ovalbumin phosphoserine peptide - fulvous whistling-duck (fragments)

C;Species: Dendrocygna bicolor (fulvous whistling-duck)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: F23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: F23454

A;Molecule type: protein

A;Residues: 1-32 <HEN>

C;Superfamily: antithrombin III

Query Match 12.9%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
|||
Db 26 SVSE 29

RESULT 14

D31461

T-cell receptor delta chain BDN7, thymus - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 30-May-1997

C;Accession: D31461

R;Lacy, M.J.; McNeil, L.K.; Roth, M.E.; Kranz, D.M.

Proc. Natl. Acad. Sci. U.S.A. 86, 1023-1026, 1989

A;Title: T-cell receptor delta-chain diversity in peripheral lymphocytes.

A;Reference number: A31461; MUID:89128840; PMID:2783779

A;Accession: D31461

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: mRNA

A;Residues: 1-32 <LAC>

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 12.9%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MERV 21
|||
Db 8 MERV 11

RESULT 15

G84161

hypothetical protein Vng0019h [imported] - Halobacterium sp. NRC-1

C;Species: Halobacterium sp. NRC-1

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: G84161
R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shukla, H.D.;
Lasky, S.R.; Baliga, N.; Thorsson, V.; Sbrogna, J.; Swartzell, S.; Weir, D.;
Hall, J.; Dahl, T.A.; Welte, R.; Goo, Y.A.; Leithauser, B.; Keller, K.; Cruz,
R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablonski, P.E.; Krebs, M.P.;
Angevine, C.M.; Dale, H.; Isenbarger, T.A.; Peck, R.F.; Pohlschrod, M.; Spudich,
J.L.; Jung, K.H.; Alam, M.; Freitas, T.
Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A;Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, H.; Lowe,
T.M.; Liang, P.; Riley, M.; Hood, L.; DasSarma, S.
A;Title: Genome sequence of Halobacterium species NRC-1.
A;Reference number: A84160; MUID:20504483; PMID:11016950
A;Accession: G84161
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-32 <STO>
A;Cross-references: GB:AE004437; NID:g10579667; PIDN:AAG18659.1; GSPDB:GN00138
C;Genetics:
A;Gene: VNG0019H

Query Match 12.9%; Score 4; DB 2; Length 32;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 13 KLQD 16

RESULT 16

E81714

hypothetical protein TC0337 [imported] - Chlamydia muridarum (strain Nigg)

C;Species: Chlamydia muridarum, Chlamydia trachomatis MoPn

C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 11-May-2000

C;Accession: E81714

R;Read, T.D.; Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.;
Hickey, E.K.; Peterson, J.; Utterback, T.; Berry, K.; Bass, S.; Linher, K.;
Weidman, J.; Khouri, H.; Craven, B.; Bowman, C.; Dodson, R.; Gwinn, M.; Nelson,
W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, S.L.; Eisen, J.; Fraser,
C.M.

Nucleic Acids Res. 28, 1397-1406, 2000

A;Title: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae
AR39.

A;Reference number: A81500; MUID:20150255; PMID:10684935

A;Accession: E81714

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-33 <TET>

A;Cross-references: GB:AE002301; GB:AE002160; NID:g7190372; PIDN:AAF39200.1;
PID:g7190379; GSPDB:GN00121; TIGR:TC0337

A;Experimental source: strain Nigg (MoPn)

C;Genetics:

A;Gene: TC0337

Query Match 12.9%; Score 4; DB 2; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKK 27
 ||||
Db 26 LRKK 29

RESULT 17

D23454

ovalbumin phosphoserine peptide - golden pheasant (fragments)

C;Species: Chrysolophus pictus (golden pheasant)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: D23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: D23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 12.9%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSE 4
 ||||
Db 29 SVSE 32

RESULT 18

G23454

ovalbumin phosphoserine peptide - magpie goose (fragments)

C;Species: Anseranas semipalmata (magpie goose)

C;Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 13-Mar-1998

C;Accession: G23454

R;Henderson, J.Y.; Moir, A.J.G.; Fothergill, L.A.; Fothergill, J.E.

Eur. J. Biochem. 114, 439-450, 1981

A;Title: Sequences of sixteen phosphoserine peptides from ovalbumins of eight species.

A;Reference number: A91106; MUID:81164535; PMID:6783411

A;Accession: G23454

A;Molecule type: protein

A;Residues: 1-35 <HEN>

C;Superfamily: antithrombin III

Query Match 12.9%; Score 4; DB 2; Length 35;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSE 4
 ||||
Db 29 SVSE 32

RESULT 19

D82125
 hypothetical protein VC2034 [imported] - *Vibrio cholerae* (strain N16961 serogroup O1)
 C;Species: *Vibrio cholerae*
 C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C;Accession: D82125
 R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey, E.K.; Peterson, J.D.; Umayam, L.A.; Gill, S.R.; Nelson, K.E.; Read, T.D.; Tettelin, H.; Richardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragoi, I.; Sellers, P.; McDonald, L.; Utterback, T.; Fleishmann, R.D.; Nierman, W.C.; White, O.; Salzberg, S.L.; Smith, H.O.; Colwell, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M. Nature 406, 477-483, 2000
 A;Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A;Reference number: A82035; MUID:20406833; PMID:10952301
 A;Accession: D82125
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-35 <HEI>
 A;Cross-references: GB:AE004278; GB:AE003852; NID:g9656579; PIDN:AAF95182.1; GSPDB:GN00126; TIGR:VC2034
 A;Experimental source: serogroup O1; strain N16961; biotype El Tor
 C;Genetics:
 A;Gene: VC2034
 A;Map position: 1

Query Match 12.9%; Score 4; DB 2; Length 35;
 Best Local Similarity 100.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 24 KKLQ 27

RESULT 20
 S70806
 hypothetical protein 5 - *Vibrio cholerae* (fragment)
 N;Alternate names: flagellar protein flaA homolog
 C;Species: *Vibrio cholerae*
 C;Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 26-Aug-1999
 C;Accession: S70806
 R;Camilli, A.; Mekalanos, J.J. Mol. Microbiol. 18, 671-683, 1995
 A;Title: Use of recombinase gene fusions to identify *Vibrio cholerae* genes induced during infection.
 A;Reference number: S70798; MUID:96414469; PMID:8817490
 A;Accession: S70806
 A;Status: preliminary; nucleic acid sequence not shown
 A;Molecule type: DNA
 A;Residues: 1-36 <CAM>
 A;Cross-references: EMBL:U25820; NID:g1165195; PIDN:AAC43560.1; PID:g1165196
 C;Superfamily: flagellin

Query Match 12.9%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 17 SMER 20
||||
Db 14 SMER 17

RESULT 21

F95057

hypothetical protein SP0497 [imported] - Streptococcus pneumoniae (strain TIGR4)

C;Species: Streptococcus pneumoniae

C;Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C;Accession: F95057

R;Tettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidelberg, J.; DeBoy, R.T.; Haft, D.H.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.; Kolonay, J.F.; Nelson, W.C.; Peterson, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, E.; Khouri, H.; Wolf, A.M.; Utterback, T.R.; Hansen, C.L.; McDonald, L.A.; Feldblyum, T.V.; Angiuoli, S.; Dickinson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, D.A.; Hollingshead, S.K.; Fraser, C.M.

A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.

A;Reference number: A95000; MUID:21357209; PMID:11463916

A;Accession: F95057

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <KUR>

A;Cross-references: GB:AE005672; PIDN:AAK74655.1; PID:g14971969; GSPDB:GN00164; TIGR:SP4SP0497

A;Experimental source: strain TIGR4

C;Genetics:

A;Gene: SP0497

Query Match 12.9%; Score 4; DB 2; Length 36;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
||||
Db 10 KKLQ 13

RESULT 22

A84774

hypothetical protein At2g35870 [imported] - Arabidopsis thaliana

C;Species: Arabidopsis thaliana (mouse-ear cress)

C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C;Accession: A84774

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; Mason, T.M.; Bowman, C.L.; Barnstead, M.E.; Feldblyum, T.V.; Buell, C.R.; Ketchum, K.A.; Lee, J.J.; Ronning, C.M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.J.; Gill, J.E.; Adams, M.D.; Carrera, A.J.; Creasy, T.H.; Goodman, H.M.; Somerville, C.R.; Copenhaver, G.P.; Preuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.

Nature 402, 761-768, 1999

A;Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.

A;Reference number: A84420; MUID:20083487; PMID:10617197

A;Accession: A84774

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-36 <STO>

A;Cross-references: GB:AE002093; NID:g4510382; PIDN:AAD21470.1; GSPDB:GN00139

C;Genetics:

A;Gene: At2g35870

A;Map position: 2

Query Match 12.9%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 4 KKLQ 7

RESULT 23

S46227

hypothetical protein - *Streptomyces chrysomallus* (fragment)

C;Species: *Streptomyces chrysomallus*

C;Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 28-May-1999

C;Accession: S46227

R;Pahl, A.; Keller, U.

EMBO J. 13, 3472-3480, 1994

A;Title: *Streptomyces chrysomallus* FKBP-33 is a novel immunophilin consisting of two FK506 binding domains; its gene is transcriptionally coupled to the FKBP-12 gene.

A;Reference number: S46227; MUID:94341259; PMID:8062824

A;Accession: S46227

A;Molecule type: DNA

A;Residues: 1-36 <PAH>

A;Cross-references: GB:Z34523; NID:g535270; PIDN:CAA84281.1; PID:g633645

A;Experimental source: strain ATCC 11523

Query Match 12.9%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 27 ERVE 30

RESULT 24

S71912

hemoglobin, extracellular, chain A1 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71912

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71912

A;Molecule type: protein

A;Residues: 1-37 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 12.9%; Score 4; DB 2; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22

||||

Db 25 ERVE 28

RESULT 25

T12635

homeotic protein HAHB-2 - common sunflower (fragment)

C;Species: *Helianthus annuus* (common sunflower)

C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 21-Jul-2000

C;Accession: T12635

R;Chan, R.L.; Gonzalez, D.H.

Plant Physiol. 106, 1687-1688, 1994

A;Title: A cDNA encoding an HD-zip protein from sunflower.

A;Reference number: Z17563; MUID:95148747; PMID:7846169

A;Accession: T12635

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-37 <CHA>

A;Cross-references: EMBL:L22849; NID:g349258; PIDN:AAA63766.1; PID:g349259

C;Keywords: DNA binding; homeobox; transcription regulation

Query Match 12.9%; Score 4; DB 2; Length 37;

Best Local Similarity 100.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28

||||

Db 6 RKKL 9

RESULT 26

CKFHCS

sarcotoxin IC - flesh fly (*Sarcophaga peregrina*)

C;Species: *Sarcophaga peregrina*

C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 08-Dec-1995

C;Accession: C22625

R;Okada, M.; Natori, S.

J. Biol. Chem. 260, 7174-7177, 1985

A;Title: Primary structure of sarcotoxin I, an antibacterial protein induced in the hemolymph of *Sarcophaga peregrina* (flesh fly) larvae.

A;Reference number: A92536; MUID:85207747; PMID:3888997
A;Accession: C22625
A;Molecule type: protein
A;Residues: 1-39 <OKA>
C;Comment: Sarcotoxins, which are potent bactericidal proteins, are produced in response to injury. They are cytotoxic to both Gram positive and Gram negative bacteria.
C;Superfamily: cecropin
C;Keywords: amidated carboxyl end; antibacterial; hemolymph
F;39/Modified site: amidated carboxyl end (Arg) #status predicted

Query Match 12.9%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
|||
Db 2 WLRK 5

RESULT 27

S71913

hemoglobin, extracellular, chain A2 - polychaete (*Perinereis aibuhitensis*) (fragment)

C;Species: *Perinereis aibuhitensis*

C;Date: 14-Apr-1998 #sequence_revision 08-May-1998 #text_change 02-Jul-1998

C;Accession: S71913

R;Matsubara, K.; Yamaki, M.; Nagayama, K.; Imai, K.; Ishii, H.; Gotoh, T.; Ebina, S.

Biochim. Biophys. Acta 1290, 215-223, 1996

A;Title: Wheat germ agglutinin-reactive chains of giant hemoglobin from the polychaete *Perinereis aibuhitensis*.

A;Reference number: S71912; MUID:96350431; PMID:8765123

A;Accession: S71913

A;Molecule type: protein

A;Residues: 1-39 <MAT>

C;Superfamily: globin; globin homology

C;Keywords: chromoprotein; heme; iron; oxygen carrier

Query Match 12.9%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
|||
Db 27 ERVE 30

RESULT 28

S77164

ycf32 protein - *Synechocystis* sp. (strain PCC 6803)

N;Alternate names: protein sml0007

C;Species: *Synechocystis* sp.

A;Variety: PCC 6803

C;Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000

C;Accession: S77164

R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; Hirose, M.; Sugiura, M.; Sasamoto, S.; Kimura, T.; Hosouchi, T.; Matsuno, A.; Muraki, A.; Nakazaki, N.; Naruo, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda, M.; Tabata, S. DNA Res. 3, 109-136, 1996

A;Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp. PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions.

A;Reference number: S74322; MUID:97061201; PMID:8905231

A;Accession: S77164

A;Status: nucleic acid sequence not shown; translation not shown

A;Molecule type: DNA

A;Residues: 1-39 <KAN>

A;Cross-references: EMBL:D90908; GB:AB001339; NID:g1652725; PIDN:BAA17722.1; PID:g1652803

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

C;Genetics:

A;Gene: ycf32

C;Superfamily: hypothetical protein ycf32

Query Match 12.9%; Score 4; DB 2; Length 39;
Best Local Similarity 100.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
|||
Db 31 LQDV 34

RESULT 29

A42272

brain-type creatine kinase, peptide B - spiny dogfish (fragment)

C;Species: *Squalus acanthias* (spiny dogfish)

C;Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1997

C;Accession: A42272

R;Friedman, D.L.; Roberts, R.

J. Biol. Chem. 267, 4270-4276, 1992

A;Title: Purification and localization of brain-type creatine kinase in sodium chloride transporting epithelia of the spiny dogfish, *Squalus acanthias*.

A;Reference number: A42272; MUID:92156175; PMID:1310991

A;Accession: A42272

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <FRI>

A;Note: sequence extracted from NCBI backbone (NCBIP:82919)

C;Superfamily: creatine kinase; creatine kinase repeat homology

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 10 KKL 12

RESULT 30

C32416

phospholipase A2 (EC 3.1.1.4) pseudexin chain C - red-bellied black snake (fragment)

C;Species: Pseudechis porphyriacus (red-bellied black snake)

C;Date: 05-Oct-1989 #sequence_revision 05-Oct-1989 #text_change 23-Jun-1993

C;Accession: C32416

R;Schmidt, J.J.; Middlebrook, J.L.

Toxicon 27, 805-818, 1989

A;Title: Purification, sequencing and characterization of pseudexin phospholipases A-2 from Pseudechis porphyriacus (Australian red-bellied black snake).

A;Reference number: A32416; MUID:89388835; PMID:2675391

A;Accession: C32416

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-28 <SCH>

C;Superfamily: phospholipase A2

C;Keywords: carboxylic ester hydrolase

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
|||
Db 3 IQL 5

RESULT 31

B60071

vasoactive intestinal peptide - rhesus macaque

C;Species: Macaca mulatta (rhesus macaque)

C;Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 20-Mar-1998

C;Accession: B60071

R;Yu, J.; Xin, Y.; Eng, J.; Yalow, R.S.

Regul. Pept. 32, 39-45, 1991

A;Title: Rhesus monkey gastroenteropancreatic hormones: relationship to human sequences.

A;Reference number: A60071; MUID:91164506; PMID:2003150

A;Accession: B60071

A;Status: protein sequence not shown

A;Molecule type: protein

A;Residues: 1-28 <YUA>

A;Note: the sequence is identical with the human sequence

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 32

A60304

vasoactive intestinal peptide - dog

N;Alternate names: VIP

C;Species: Canis lupus familiaris (dog)

C;Date: 15-Jan-1993 #sequence_revision 15-Jan-1993 #text_change 20-Mar-1998

C;Accession: A60304

R;Eng, J.; Pan, Y.C.E.; Raufman, J.P.; Yalow, R.S.

Regul. Pept. Suppl. 3, S14, 1985

A;Title: Purification and sequencing of dog and guinea pig VIP's.

A;Reference number: A60304

A;Accession: A60304

A;Molecule type: protein

A;Residues: 1-28 <ENG>

C;Superfamily: glucagon

C;Keywords: duplication; hormone; intestine; neuropeptide; vasodilator

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 33

S58386

T-cell receptor beta-chain Vb11-Jb2.4 - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 29-Nov-1995 #sequence_revision 01-Mar-1996 #text_change 23-Jul-1999

C;Accession: S58386

R;Johnston, S.L.; Strausbauch, M.; Sarkar, G.; Wettstein, P.J.

Nucleic Acids Res. 23, 3074-3075, 1995

A;Title: A novel method for sequencing members of multi-gene families.

A;Reference number: S58384; MUID:95388532; PMID:7659534

A;Accession: S58386

A;Status: preliminary; nucleic acid sequence not shown

A;Molecule type: mRNA

A;Residues: 1-28 <JOH>

A;Cross-references: EMBL:U20300; NID:g663123; PIDN:AAA62247.1; PID:g663124

A;Note: the nucleotide sequence was submitted to the EMBL Data Library, January 1995

A;Note: only a part of the coding sequence is given

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: T-cell receptor

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
|||
Db 12 ERV 14

RESULT 34

PN0047
signal transduction protein QM0017 - mouse (fragments)
C;Species: Mus musculus (house mouse)
C;Date: 29-Oct-1997 #sequence_revision 29-Oct-1997 #text_change 15-Oct-1999
C;Accession: PN0047
R;Kato, H.
Kawasaki Igakkaishi 22, 245-259, 1996
A;Title: Analysis of proteins isolated by two dimensional electrophoresis of mouse neuroblastoma cells.
A;Reference number: PN0041
A;Accession: PN0047
A;Molecule type: protein
A;Residues: 1-28 <KAT>
A;Experimental source: neuroblastoma cell
C;Comment: The molecular mass is 25,600 and the pI is 6.07. The amino-terminus is blocked.
C;Superfamily: signal transduction protein DJ-1
C;Keywords: brain

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
|||
Db 14 NLG 16

RESULT 35

S70894

hypothetical protein 1 - Vibrio anguillarum (fragment)
C;Species: Vibrio anguillarum
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 08-Oct-1999
C;Accession: S70894
R;O'Toole, R.; Milton, D.L.; Wolf-Watz, H.
Mol. Microbiol. 19, 625-637, 1996
A;Title: Chemotactic motility is required for invasion of the host by the fish pathogen Vibrio anguillarum.
A;Reference number: S70894; MUID:96228710; PMID:8830252
A;Accession: S70894
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <OTO>
A;Cross-references: GB:U36378; EMBL:L47344; NID:g1020321; PIDN:AAB38488.1; PID:g1723992

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 18 LNS 20

RESULT 36

S22469

hypothetical protein 1 - Prochlorothrix hollandica
C;Species: Prochlorothrix hollandica
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 15-Oct-1999
C;Accession: S22469; S16850
R;Greer, K.L.; Golden, S.S.
Plant Mol. Biol. 19, 355-365, 1992
A;Title: Conserved relationship between psbH and petBD genes: presence of a shared upstream element in Prochlorothrix hollandica.
A;Reference number: S22469; MUID:92322967; PMID:1623188
A;Accession: S22469
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-28 <GRE>
A;Cross-references: EMBL:X60313; NID:g45528; PIDN:CAA42858.1; PID:g45529

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVS 3
|||
Db 4 SVS 6

RESULT 37

S26254
rel protein - chicken
C;Species: Gallus gallus (chicken)
C;Date: 25-Feb-1994 #sequence_revision 10-Nov-1995 #text_change 06-Dec-1996
C;Accession: S26254
R;Capobianco, A.J.; Gilmore, T.D.
Oncogene 6, 2203-2210, 1991
A;Title: Repression of the chicken c-rel promoter by vRel in chicken embryo fibroblasts is not mediated through a consensus NF-kappaB binding site.
A;Reference number: S26254; MUID:92115319; PMID:1766669
A;Accession: S26254
A;Status: preliminary; translation not shown
A;Molecule type: DNA
A;Residues: 1-28 <CAP>
A;Cross-references: EMBL:X59588

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 20 RVE 22
|||
Db 1 RVE 3

RESULT 38

I59477
antigen, T-cell receptor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C;Accession: I59477
R;Mathioudakis, G.; Chen, P.

Scand. J. Immunol. 38, 31-36, 1993

A;Title: Preferential rearrangements of the V gamma I subgroup of the gamma-chain of the T-cell antigen receptor to J gamma 2C gamma 2 gene segments in peripheral blood lymphocyte transcripts from normal donors.

A;Reference number: I59477; MUID:93318104; PMID:8392223

A;Accession: I59477

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: mRNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:M89844; NID:g181657; PIDN:AAA02695.1; PID:g181658

C;Keywords: T-cell receptor

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 10 KKL 12

RESULT 39

F46522

T-cell receptor eta chain - rat (fragment)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C;Accession: F46522; I56191

R;Jensen, J.P.; Cenciarelli, C.; Hou, D.; Rellahan, B.L.; Dean, M.; Weissman, A.M.

J. Immunol. 150, 122-130, 1993

A;Title: T cell antigen receptor-eta subunit. Low levels of expression and limited cross-species conservation.

A;Reference number: A46522; MUID:93107707; PMID:8417118

A;Accession: F46522

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: nucleic acid

A;Residues: 1-28 <JEN>

A;Cross-references: GB:S51404; NID:g262180; PIDN:AAB24606.1; PID:g262181

A;Note: sequence extracted from NCBI backbone (NCBIP:120909)

R;Itoh, Y.; Matsuura, A.; Kinebuchi, M.; Honda, R.; Takayama, S.; Ichimiya, S.; Kon, S.; Kikuchi, K.

J. Immunol. 151, 4705-4717, 1993

A;Title: Structural analysis of the CD3 zeta/eta locus of the rat. Expression of zeta but eta transcripts by rat T cells.

A;Reference number: I56191; MUID:94014415; PMID:8409430

A;Accession: I56191

A;Status: preliminary; translated from GB/EMBL/DDBJ

A;Molecule type: DNA

A;Residues: 1-28 <RES>

A;Cross-references: GB:D13556; NID:g436580; PIDN:BAA02754.1; PID:g436581

C;Keywords: T-cell receptor

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27

Db |||
 13 RKK 15

RESULT 40

H85908

hypothetical protein Z3917 [imported] - Escherichia coli (strain O157:H7, substrain EDL933)

C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C;Accession: H85908

R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayhew, G.F.; Evans, P.S.; Gregor, J.; Kirkpatrick, H.A.; Posfai, G.; Hackett, J.; Klink, S.; Boutin, A.; Shao, Y.; Miller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodaca, J.; Anantharaman, T.S.; Lin, J.; Yen, G.; Schwartz, D.C.; Welch, R.A.; Blattner, F.R.

Nature 409, 529-533, 2001

A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A;Reference number: A85480; MUID:21074935; PMID:11206551

A;Accession: H85908

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-28 <STO>

A;Cross-references: GB:AE005174; NID:gl2517049; PIDN:AAG57732.1; GSPDB:GN00145; UWGP:Z3917

A;Experimental source: strain O157:H7, substrain EDL933

C;Genetics:

A;Gene: Z3917

Query Match 9.7%; Score 3; DB 2; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQD 30

Db |||
 9 LQD 11

Search completed: January 14, 2004, 10:37:26

Job time : 11.1745 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:37:44 ; Search time 20.8598 Seconds
(without alignments)
303.882 Million cell updates/sec

Title: US-09-843-221A-165
Perfect score: 31
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 762491 seqs, 204481190 residues

Word size : 0

Total number of hits satisfying chosen parameters: 28045

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : Published_Applications_AA:*
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query				
No.	Score	Match	Length	DB	ID	Description

1	31	100.0	31	9	US-09-169-786-2	Sequence 2, Appli
2	31	100.0	31	11	US-09-843-221A-27	Sequence 27, Appl
3	31	100.0	31	11	US-09-843-221A-165	Sequence 165, App
4	31	100.0	33	12	US-10-361-928-9	Sequence 9, Appli
5	31	100.0	34	9	US-09-169-786-3	Sequence 3, Appli
6	31	100.0	34	10	US-09-928-047B-6	Sequence 6, Appli
7	31	100.0	34	11	US-09-843-221A-16	Sequence 16, Appl
8	31	100.0	34	11	US-09-843-221A-161	Sequence 161, App
9	31	100.0	34	12	US-09-928-048A-6	Sequence 6, Appli
10	31	100.0	34	12	US-10-361-928-8	Sequence 8, Appli
11	31	100.0	34	12	US-10-340-484-15	Sequence 15, Appl
12	31	100.0	34	12	US-10-340-484-16	Sequence 16, Appl
13	31	100.0	34	14	US-10-016-403-5	Sequence 5, Appli
14	31	100.0	34	14	US-10-097-079-1	Sequence 1, Appli
15	31	100.0	37	12	US-10-168-185-9	Sequence 9, Appli
16	31	100.0	38	9	US-09-169-786-4	Sequence 4, Appli
17	31	100.0	38	11	US-09-843-221A-14	Sequence 14, Appl
18	31	100.0	38	12	US-10-245-707-1	Sequence 1, Appli
19	30	96.8	30	11	US-09-843-221A-39	Sequence 39, Appl
20	30	96.8	30	11	US-09-843-221A-166	Sequence 166, App
21	30	96.8	33	12	US-10-361-928-3	Sequence 3, Appli
22	30	96.8	33	12	US-10-361-928-6	Sequence 6, Appli
23	30	96.8	34	11	US-09-843-221A-20	Sequence 20, Appl
24	30	96.8	34	12	US-10-361-928-1	Sequence 1, Appli
25	30	96.8	34	12	US-10-361-928-2	Sequence 2, Appli
26	30	96.8	34	12	US-10-361-928-5	Sequence 5, Appli
27	30	96.8	37	11	US-09-843-221A-15	Sequence 15, Appl
28	29	93.5	29	11	US-09-843-221A-51	Sequence 51, Appl
29	29	93.5	29	11	US-09-843-221A-167	Sequence 167, App
30	29	93.5	30	11	US-09-843-221A-43	Sequence 43, Appl
31	28	90.3	28	11	US-09-843-221A-52	Sequence 52, Appl
32	28	90.3	28	11	US-09-843-221A-168	Sequence 168, App
33	28	90.3	34	12	US-10-372-095-24	Sequence 24, Appl
34	28	90.3	34	14	US-10-016-403-7	Sequence 7, Appli
35	26	83.9	30	11	US-09-843-221A-50	Sequence 50, Appl
36	26	83.9	31	11	US-09-843-221A-28	Sequence 28, Appl
37	26	83.9	31	12	US-10-031-874A-206	Sequence 206, App
38	25	80.6	28	11	US-09-843-221A-32	Sequence 32, Appl
39	25	80.6	34	14	US-10-016-403-6	Sequence 6, Appli
40	22	71.0	30	11	US-09-843-221A-124	Sequence 124, App
41	22	71.0	30	11	US-09-843-221A-125	Sequence 125, App
42	22	71.0	34	11	US-09-843-221A-88	Sequence 88, Appl
43	22	71.0	34	11	US-09-843-221A-89	Sequence 89, Appl
44	21	67.7	30	11	US-09-843-221A-126	Sequence 126, App
45	21	67.7	30	11	US-09-843-221A-127	Sequence 127, App
46	21	67.7	34	11	US-09-843-221A-90	Sequence 90, Appl
47	21	67.7	34	11	US-09-843-221A-91	Sequence 91, Appl
48	21	67.7	34	11	US-09-843-221A-92	Sequence 92, Appl
49	21	67.7	34	11	US-09-843-221A-128	Sequence 128, App
50	20	64.5	34	11	US-09-843-221A-17	Sequence 17, Appl
51	20	64.5	34	11	US-09-843-221A-18	Sequence 18, Appl
52	20	64.5	34	11	US-09-843-221A-162	Sequence 162, App
53	20	64.5	34	11	US-09-843-221A-163	Sequence 163, App
54	19	61.3	30	11	US-09-843-221A-40	Sequence 40, Appl
55	19	61.3	30	11	US-09-843-221A-41	Sequence 41, Appl
56	18	58.1	30	11	US-09-843-221A-42	Sequence 42, Appl

57	18	58.1	34	11	US-09-843-221A-19	Sequence 19, Appl
58	18	58.1	34	11	US-09-843-221A-164	Sequence 164, App
59	17	54.8	34	12	US-10-340-484-17	Sequence 17, Appl
60	16	51.6	28	11	US-09-843-221A-93	Sequence 93, Appl
61	16	51.6	28	11	US-09-843-221A-94	Sequence 94, Appl
62	15	48.4	28	11	US-09-843-221A-34	Sequence 34, Appl
63	15	48.4	28	11	US-09-843-221A-35	Sequence 35, Appl
64	15	48.4	28	11	US-09-843-221A-95	Sequence 95, Appl
65	15	48.4	28	11	US-09-843-221A-96	Sequence 96, Appl
66	15	48.4	28	11	US-09-843-221A-97	Sequence 97, Appl
67	15	48.4	30	11	US-09-843-221A-47	Sequence 47, Appl
68	15	48.4	32	11	US-09-843-221A-30	Sequence 30, Appl
69	15	48.4	34	11	US-09-843-221A-22	Sequence 22, Appl
70	15	48.4	34	11	US-09-843-221A-24	Sequence 24, Appl
71	15	48.4	34	12	US-10-340-484-18	Sequence 18, Appl
72	15	48.4	34	12	US-10-340-484-19	Sequence 19, Appl
73	15	48.4	34	12	US-10-340-484-20	Sequence 20, Appl
74	15	48.4	40	15	US-10-014-162-111	Sequence 111, App
75	14	45.2	28	11	US-09-843-221A-54	Sequence 54, Appl
76	14	45.2	30	11	US-09-843-221A-45	Sequence 45, Appl
77	14	45.2	30	11	US-09-843-221A-48	Sequence 48, Appl
78	14	45.2	34	11	US-09-843-221A-25	Sequence 25, Appl
79	14	45.2	34	12	US-10-340-484-22	Sequence 22, Appl
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83	13	41.9	32	11	US-09-843-221A-29	Sequence 29, Appl
84	13	41.9	32	11	US-09-843-221A-31	Sequence 31, Appl
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86	13	41.9	34	11	US-09-843-221A-21	Sequence 21, Appl
87	13	41.9	34	11	US-09-843-221A-23	Sequence 23, Appl
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89	12	38.7	28	11	US-09-843-221A-55	Sequence 55, Appl
90	12	38.7	30	11	US-09-843-221A-44	Sequence 44, Appl
91	12	38.7	30	11	US-09-843-221A-46	Sequence 46, Appl
92	10	32.3	31	9	US-09-169-786-9	Sequence 9, Appli
93	9	29.0	28	14	US-10-097-079-54	Sequence 54, Appl
94	9	29.0	28	14	US-10-097-079-62	Sequence 62, Appl
95	9	29.0	28	14	US-10-097-079-65	Sequence 65, Appl
96	9	29.0	28	14	US-10-097-079-79	Sequence 79, Appl
97	9	29.0	29	14	US-10-097-079-53	Sequence 53, Appl
98	9	29.0	29	14	US-10-097-079-63	Sequence 63, Appl
99	9	29.0	30	14	US-10-097-079-52	Sequence 52, Appl
100	9	29.0	30	14	US-10-097-079-64	Sequence 64, Appl
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105	9	29.0	31	14	US-10-097-079-7	Sequence 7, Appli
106	9	29.0	31	14	US-10-097-079-8	Sequence 8, Appli
107	9	29.0	31	14	US-10-097-079-9	Sequence 9, Appli
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111	9	29.0	31	14	US-10-097-079-22	Sequence 22, Appl
112	9	29.0	31	14	US-10-097-079-23	Sequence 23, Appl
113	9	29.0	31	14	US-10-097-079-24	Sequence 24, Appl

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121	9	29.0	31	14	US-10-097-079-47	Sequence 47, Appl
122	9	29.0	31	14	US-10-097-079-48	Sequence 48, Appl
123	9	29.0	31	14	US-10-097-079-49	Sequence 49, Appl
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125	9	29.0	31	14	US-10-097-079-51	Sequence 51, Appl
126	9	29.0	31	14	US-10-097-079-69	Sequence 69, Appl
127	9	29.0	31	14	US-10-097-079-70	Sequence 70, Appl
128	9	29.0	31	14	US-10-097-079-74	Sequence 74, Appl
129	9	29.0	31	14	US-10-097-079-81	Sequence 81, Appl
130	9	29.0	31	14	US-10-097-079-82	Sequence 82, Appl
131	9	29.0	31	14	US-10-097-079-83	Sequence 83, Appl
132	9	29.0	31	14	US-10-097-079-84	Sequence 84, Appl
133	9	29.0	31	14	US-10-097-079-85	Sequence 85, Appl
134	9	29.0	34	11	US-09-843-221A-26	Sequence 26, Appl
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136	9	29.0	34	14	US-10-097-079-46	Sequence 46, Appl
137	8	25.8	28	14	US-10-097-079-78	Sequence 78, Appl
138	8	25.8	30	11	US-09-843-221A-49	Sequence 49, Appl
139	8	25.8	30	11	US-09-843-221A-158	Sequence 158, App
140	8	25.8	30	11	US-09-843-221A-159	Sequence 159, App
141	8	25.8	31	9	US-09-169-786-10	Sequence 10, Appl
142	8	25.8	31	14	US-10-097-079-11	Sequence 11, Appl
143	8	25.8	31	14	US-10-097-079-19	Sequence 19, Appl
144	8	25.8	31	14	US-10-097-079-28	Sequence 28, Appl
145	8	25.8	31	14	US-10-097-079-35	Sequence 35, Appl
146	8	25.8	31	14	US-10-097-079-40	Sequence 40, Appl
147	8	25.8	31	14	US-10-097-079-45	Sequence 45, Appl
148	8	25.8	31	14	US-10-097-079-66	Sequence 66, Appl
149	8	25.8	31	14	US-10-097-079-67	Sequence 67, Appl
150	8	25.8	31	14	US-10-097-079-68	Sequence 68, Appl
151	8	25.8	31	14	US-10-097-079-73	Sequence 73, Appl
152	8	25.8	31	14	US-10-097-079-76	Sequence 76, Appl
153	8	25.8	31	14	US-10-097-079-80	Sequence 80, Appl
154	8	25.8	34	11	US-09-843-221A-122	Sequence 122, App
155	8	25.8	34	11	US-09-843-221A-123	Sequence 123, App
156	8	25.8	34	14	US-10-097-079-75	Sequence 75, Appl
157	7	22.6	31	14	US-10-097-079-12	Sequence 12, Appl
158	7	22.6	31	14	US-10-097-079-18	Sequence 18, Appl
159	7	22.6	31	14	US-10-097-079-29	Sequence 29, Appl
160	7	22.6	31	14	US-10-097-079-34	Sequence 34, Appl
161	7	22.6	31	14	US-10-097-079-41	Sequence 41, Appl
162	7	22.6	31	14	US-10-097-079-44	Sequence 44, Appl
163	7	22.6	34	12	US-10-340-484-24	Sequence 24, Appl
164	6	19.4	30	11	US-09-843-221A-77	Sequence 77, Appl
165	6	19.4	31	14	US-10-097-079-13	Sequence 13, Appl
166	6	19.4	31	14	US-10-097-079-14	Sequence 14, Appl
167	6	19.4	31	14	US-10-097-079-15	Sequence 15, Appl
168	6	19.4	31	14	US-10-097-079-16	Sequence 16, Appl
169	6	19.4	31	14	US-10-097-079-17	Sequence 17, Appl
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172	6	19.4	31	14	US-10-097-079-32	Sequence 32, Appl
173	6	19.4	31	14	US-10-097-079-33	Sequence 33, Appl
174	6	19.4	31	14	US-10-097-079-42	Sequence 42, Appl
175	6	19.4	31	14	US-10-097-079-43	Sequence 43, Appl
176	6	19.4	31	14	US-10-097-079-86	Sequence 86, Appl
177	6	19.4	31	14	US-10-097-079-87	Sequence 87, Appl
178	6	19.4	31	14	US-10-097-079-88	Sequence 88, Appl
179	6	19.4	36	11	US-09-843-221A-65	Sequence 65, Appl
180	5	16.1	28	11	US-09-843-221A-69	Sequence 69, Appl
181	5	16.1	28	11	US-09-843-221A-169	Sequence 169, App
182	5	16.1	34	9	US-09-864-761-38558	Sequence 38558, A
183	5	16.1	34	12	US-10-317-832-178	Sequence 178, App
184	5	16.1	38	9	US-09-864-761-49110	Sequence 49110, A
185	4	12.9	28	9	US-09-864-761-37690	Sequence 37690, A
186	4	12.9	28	9	US-09-929-818-122	Sequence 122, App
187	4	12.9	28	9	US-09-929-818-200	Sequence 200, App
188	4	12.9	28	10	US-09-003-869-153	Sequence 153, App
189	4	12.9	28	10	US-09-999-745-38	Sequence 38, Appl
190	4	12.9	28	10	US-09-554-000-22	Sequence 22, Appl
191	4	12.9	28	11	US-09-756-690A-153	Sequence 153, App
192	4	12.9	28	11	US-09-776-724A-198	Sequence 198, App
193	4	12.9	28	11	US-09-899-495-104	Sequence 104, App
194	4	12.9	28	12	US-10-029-386-28289	Sequence 28289, A
195	4	12.9	28	15	US-10-157-224A-153	Sequence 153, App
196	4	12.9	28	15	US-10-187-051-153	Sequence 153, App
197	4	12.9	29	9	US-09-730-379B-5	Sequence 5, Appli
198	4	12.9	29	11	US-09-983-802-386	Sequence 386, App
199	4	12.9	29	11	US-09-983-802-480	Sequence 480, App
200	4	12.9	29	11	US-09-969-730-133	Sequence 133, App
201	4	12.9	29	11	US-09-095-478-24	Sequence 24, Appl
202	4	12.9	29	12	US-09-933-767-1006	Sequence 1006, Ap
203	4	12.9	29	15	US-10-023-282-1006	Sequence 1006, Ap
204	4	12.9	29	15	US-10-106-698-5404	Sequence 5404, Ap
205	4	12.9	29	15	US-10-197-954-111	Sequence 111, App
206	4	12.9	30	9	US-09-864-761-41441	Sequence 41441, A
207	4	12.9	30	9	US-09-864-761-46868	Sequence 46868, A
208	4	12.9	30	10	US-09-756-983-20	Sequence 20, Appl
209	4	12.9	30	11	US-09-774-639-191	Sequence 191, App
210	4	12.9	30	12	US-09-911-261A-20	Sequence 20, Appl
211	4	12.9	30	12	US-10-310-113-19	Sequence 19, Appl
212	4	12.9	30	12	US-09-933-767-821	Sequence 821, App
213	4	12.9	30	12	US-10-173-551-40	Sequence 40, Appl
214	4	12.9	30	15	US-10-188-947-11	Sequence 11, Appl
215	4	12.9	30	15	US-10-057-408-20	Sequence 20, Appl
216	4	12.9	30	15	US-10-023-282-821	Sequence 821, App
217	4	12.9	31	9	US-09-864-761-38725	Sequence 38725, A
218	4	12.9	31	9	US-09-864-761-40464	Sequence 40464, A
219	4	12.9	31	9	US-09-864-761-44182	Sequence 44182, A
220	4	12.9	31	10	US-09-738-626-6281	Sequence 6281, Ap
221	4	12.9	31	12	US-10-360-053-20	Sequence 20, Appl
222	4	12.9	31	12	US-09-933-767-1001	Sequence 1001, Ap
223	4	12.9	31	12	US-10-029-386-32285	Sequence 32285, A
224	4	12.9	31	12	US-10-264-049-3767	Sequence 3767, Ap
225	4	12.9	31	15	US-10-023-282-1001	Sequence 1001, Ap
226	4	12.9	31	15	US-10-106-698-7956	Sequence 7956, Ap
227	4	12.9	32	9	US-09-864-761-48632	Sequence 48632, A

228	4	12.9	32	9	US-09-281-717-16	Sequence 16, Appl
229	4	12.9	32	11	US-09-809-391-442	Sequence 442, App
230	4	12.9	32	12	US-09-882-171-442	Sequence 442, App
231	4	12.9	32	12	US-10-310-113-23	Sequence 23, Appl
232	4	12.9	32	12	US-10-310-113-134	Sequence 134, App
233	4	12.9	32	12	US-10-310-113-135	Sequence 135, App
234	4	12.9	32	12	US-10-310-113-136	Sequence 136, App
235	4	12.9	32	12	US-10-164-279-39	Sequence 39, Appl
236	4	12.9	32	12	US-10-164-279-43	Sequence 43, Appl
237	4	12.9	32	15	US-10-174-410-212	Sequence 212, App
238	4	12.9	33	9	US-09-864-761-35714	Sequence 35714, A
239	4	12.9	33	9	US-09-864-761-48253	Sequence 48253, A
240	4	12.9	33	9	US-09-864-761-49019	Sequence 49019, A
241	4	12.9	33	9	US-09-925-299-1526	Sequence 1526, Ap
242	4	12.9	33	11	US-09-925-299-1526	Sequence 1526, App
243	4	12.9	33	11	US-09-809-391-660	Sequence 660, App
244	4	12.9	33	12	US-09-882-171-660	Sequence 660, App
245	4	12.9	33	12	US-09-933-767-368	Sequence 368, App
246	4	12.9	33	12	US-10-164-279-63	Sequence 63, Appl
247	4	12.9	33	14	US-10-215-297-4	Sequence 4, Appli
248	4	12.9	33	15	US-10-215-298-4	Sequence 4, Appli
249	4	12.9	33	15	US-10-081-816-110	Sequence 110, App
250	4	12.9	33	15	US-10-023-282-368	Sequence 368, App
251	4	12.9	34	9	US-09-864-761-44185	Sequence 44185, A
252	4	12.9	34	9	US-09-864-761-44916	Sequence 44916, A
253	4	12.9	34	9	US-09-864-761-45430	Sequence 45430, A
254	4	12.9	34	9	US-09-864-761-48511	Sequence 48511, A
255	4	12.9	34	12	US-10-231-417-538	Sequence 538, App
256	4	12.9	34	12	US-10-029-386-27795	Sequence 27795, A
257	4	12.9	34	15	US-10-106-698-8037	Sequence 8037, Ap
258	4	12.9	35	9	US-09-925-299-1258	Sequence 1258, Ap
259	4	12.9	35	10	US-09-811-824-7	Sequence 7, Appli
260	4	12.9	35	11	US-09-983-802-486	Sequence 486, App
261	4	12.9	35	11	US-09-820-843A-106	Sequence 106, App
262	4	12.9	35	11	US-09-925-299-1258	Sequence 1258, Ap
263	4	12.9	35	12	US-10-289-660-75	Sequence 75, Appl
264	4	12.9	35	12	US-10-340-484-13	Sequence 13, Appl
265	4	12.9	35	12	US-10-012-952A-147	Sequence 147, App
266	4	12.9	35	12	US-10-062-599-138	Sequence 138, App
267	4	12.9	35	15	US-10-133-128-75	Sequence 75, Appl
268	4	12.9	35	15	US-10-062-831-138	Sequence 138, App
269	4	12.9	36	8	US-08-851-965-24	Sequence 24, Appl
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271	4	12.9	36	9	US-09-864-761-39771	Sequence 39771, A
272	4	12.9	36	9	US-09-864-761-46707	Sequence 46707, A
273	4	12.9	36	9	US-09-864-761-48628	Sequence 48628, A
274	4	12.9	36	10	US-09-454-533-30	Sequence 30, Appl
275	4	12.9	36	12	US-10-340-484-12	Sequence 12, Appl
276	4	12.9	36	14	US-10-002-344A-205	Sequence 205, App
277	4	12.9	36	15	US-10-050-704-192	Sequence 192, App
278	4	12.9	37	8	US-08-851-965-22	Sequence 22, Appl
279	4	12.9	37	8	US-08-851-965-23	Sequence 23, Appl
280	4	12.9	37	8	US-08-851-965-25	Sequence 25, Appl
281	4	12.9	37	8	US-08-851-965-26	Sequence 26, Appl
282	4	12.9	37	8	US-08-851-965-27	Sequence 27, Appl
283	4	12.9	37	9	US-09-758-318-16	Sequence 16, Appl
284	4	12.9	37	9	US-09-864-761-38287	Sequence 38287, A

285	4	12.9	37	9	US-09-864-761-41884	Sequence 41884, A
286	4	12.9	37	9	US-09-864-761-42087	Sequence 42087, A
287	4	12.9	37	10	US-09-908-805B-79	Sequence 79, Appl
288	4	12.9	37	10	US-09-454-533-6	Sequence 6, Appli
289	4	12.9	37	10	US-09-454-533-28	Sequence 28, Appl
290	4	12.9	37	10	US-09-454-533-29	Sequence 29, Appl
291	4	12.9	37	10	US-09-454-533-31	Sequence 31, Appl
292	4	12.9	37	10	US-09-454-533-32	Sequence 32, Appl
293	4	12.9	37	10	US-09-454-533-33	Sequence 33, Appl
294	4	12.9	37	11	US-09-764-872-347	Sequence 347, App
295	4	12.9	37	12	US-10-340-783-16	Sequence 16, Appl
296	4	12.9	37	12	US-10-012-952A-209	Sequence 209, App
297	4	12.9	37	12	US-10-339-740-265	Sequence 265, App
298	4	12.9	37	12	US-10-283-403-9	Sequence 9, Appli
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314	4	12.9	39	15	US-10-187-051-25	Sequence 25, Appl
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857	3	9.7	29	9	US-09-904-380-23	Sequence 23, Appl
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860	3	9.7	29	9	US-09-844-353A-71	Sequence 71, Appl
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863	3	9.7	29	9	US-09-864-761-34337	Sequence 34337, A
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868	3	9.7	29	9	US-09-864-761-37814	Sequence 37814, A
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917	3	9.7	29	10	US-09-922-261-258	Sequence 258, App
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919	3	9.7	29	10	US-09-908-664-9	Sequence 9, Appli
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923	3	9.7	29	10	US-09-003-869-79	Sequence 79, Appl
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926	3	9.7	29	10	US-09-880-149-52	Sequence 52, Appl
927	3	9.7	29	10	US-09-880-149-55	Sequence 55, Appl
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929	3	9.7	29	10	US-09-867-852-152	Sequence 152, App
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931	3	9.7	29	10	US-09-071-838-242	Sequence 242, App
932	3	9.7	29	10	US-09-956-206A-1	Sequence 1, Appli
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944	3	9.7	29	11	US-09-843-221A-152	Sequence 152, App
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948	3	9.7	29	11	US-09-966-262-227	Sequence 227, App
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956	3	9.7	29	11	US-09-305-736-406	Sequence 406, App
957	3	9.7	29	11	US-09-305-736-512	Sequence 512, App
958	3	9.7	29	11	US-09-305-736-529	Sequence 529, App
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961	3	9.7	29	11	US-09-908-139-19	Sequence 19, Appl
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969	3	9.7	29	12	US-10-231-894-44	Sequence 44, Appl
970	3	9.7	29	12	US-10-345-281-52	Sequence 52, Appl
971	3	9.7	29	12	US-10-345-281-55	Sequence 55, Appl
972	3	9.7	29	12	US-10-234-816-95	Sequence 95, Appl
973	3	9.7	29	12	US-09-789-831-13	Sequence 13, Appl
974	3	9.7	29	12	US-09-935-384-757	Sequence 757, App
975	3	9.7	29	12	US-09-935-384-758	Sequence 758, App
976	3	9.7	29	12	US-10-131-909A-4	Sequence 4, Appli
977	3	9.7	29	12	US-10-131-909A-7	Sequence 7, Appli
978	3	9.7	29	12	US-10-096-777-1	Sequence 1, Appli
979	3	9.7	29	12	US-10-008-524A-123	Sequence 123, App
980	3	9.7	29	12	US-10-340-458-4	Sequence 4, Appli
981	3	9.7	29	12	US-10-340-458-21	Sequence 21, Appl
982	3	9.7	29	12	US-09-933-767-1182	Sequence 1182, Ap
983	3	9.7	29	12	US-09-963-693-71	Sequence 71, Appl
984	3	9.7	29	12	US-10-105-232-319	Sequence 319, App
985	3	9.7	29	12	US-10-105-232-512	Sequence 512, App
986	3	9.7	29	12	US-10-280-066-334	Sequence 334, App
987	3	9.7	29	12	US-10-289-135A-25	Sequence 25, Appl
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995	3	9.7	29	12	US-10-029-386-32473	Sequence 32473, A
996	3	9.7	29	12	US-10-029-386-33620	Sequence 33620, A
997	3	9.7	29	12	US-10-189-437-306	Sequence 306, App
998	3	9.7	29	12	US-10-189-437-499	Sequence 499, App
999	3	9.7	29	12	US-10-189-437-641	Sequence 641, App
1000	3	9.7	29	12	US-10-189-437-693	Sequence 693, App

ALIGNMENTS

RESULT 1

US-09-169-786-2

; Sequence 2, Application US/09169786B

; Patent No. US20020025929A1

; GENERAL INFORMATION:

; APPLICANT: Sato, Masahiko

; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE

; FILE REFERENCE: X-11480

; CURRENT APPLICATION NUMBER: US/09/169,786B

; CURRENT FILING DATE: 1998-10-09

; EARLIER APPLICATION NUMBER: US 60/061,800

; EARLIER FILING DATE: 1997-10-14

; NUMBER OF SEQ ID NOS: 12

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 2

; LENGTH: 31

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-169-786-2

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; Sequence 27, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
;   APPLICANT: KOSTENUIK, PAUL
;   APPLICANT: LIU, CHUAN-FA
;   APPLICANT: LACEY, DAVID LEE
;   TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
;   TITLE OF INVENTION: RELATED PROTEIN
;   FILE REFERENCE: A-665B
;   CURRENT APPLICATION NUMBER: US/09/843,221A
;   CURRENT FILING DATE: 2001-04-26
;   PRIOR APPLICATION NUMBER: 60/266,673
;   PRIOR FILING DATE: 2001-02-06
;   PRIOR APPLICATION NUMBER: 60/214,860
;   PRIOR FILING DATE: 2000-06-28
;   PRIOR APPLICATION NUMBER: 60/200,053
;   PRIOR FILING DATE: 2000-04-27
;   NUMBER OF SEQ ID NOS: 170
;   SOFTWARE: PatentIn version 3.1
; SEQ ID NO 27
;   LENGTH: 31
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-843-221A-27

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; Sequence 165, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN

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; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 165
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (31)..(31)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-165
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Best Local Similarity 100.0%;  Pred. No. 1.1e-24;
Matches 31;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;
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RESULT 4

US-10-361-928-9

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; Sequence 9, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
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; LENGTH: 33
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
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; Sequence 3, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-169-786-3
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; Sequence 6, Application US/09928047B
; Patent No. US20020160945A1
; GENERAL INFORMATION:
; APPLICANT: Cantor, Thomas
; TITLE OF INVENTION: CYCLASE INHIBITING PARATHYROID HORMONE
; TITLE OF INVENTION: ANTAGONIST OR MODULATORS AND OSTEOPOROSIS
; FILE REFERENCE: 53221-20002.00
; CURRENT APPLICATION NUMBER: US/09/928,047B
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: US 60/224,446
; PRIOR FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 6
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; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-928-047B-6

Query Match 100.0%; Score 31; DB 10; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
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US-09-843-221A-16
; Sequence 16, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-16

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Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

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US-09-843-221A-161
; Sequence 161, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL

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; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 161
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (34)..(34)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-161

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Query Match          100.0%;  Score 31;  DB 11;  Length 34;
Best Local Similarity 100.0%;  Pred. No. 1.2e-24;
Matches 31;  Conservative 0;  Mismatches 0;  Indels 0;  Gaps 0;

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RESULT 9

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US-09-928-048A-6
; Sequence 6, Application US/09928048A
; Publication No. US20030138858A1
; GENERAL INFORMATION:
; APPLICANT: Scantibodies Laboratory, Inc.
; APPLICANT: Cantor, Thomas L.
; TITLE OF INVENTION: METHODS AND DEVICES FOR DIRECT
; TITLE OF INVENTION: DETERMINATION OF CYCLASE INHIBITING PARATHYROID HORMONE
; FILE REFERENCE: 53221-20015.00
; CURRENT APPLICATION NUMBER: US/09/928,048A
; CURRENT FILING DATE: 2000-08-10
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: PRT
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US-09-928-048A-6

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Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
```

RESULT 10

US-10-361-928-8

; Sequence 8, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ser
US-10-361-928-8

Query Match 100.0%; Score 31; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
          ||||||||||||||||||||||||||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
```

RESULT 11

US-10-340-484-15

; Sequence 15, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10

; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-340-484-15

Query Match 100.0%; Score 31; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 12

US-10-340-484-16

; Sequence 16, Application US/10340484
; Publication No. US20030171288A1
; GENERAL INFORMATION:
; APPLICANT: Stewart, Andrew F.
; TITLE OF INVENTION: Treatment of Bone Disorders with Skelatal Anabolic
; TITLE OF INVENTION: Drugs
; FILE REFERENCE: 25200-501
; CURRENT APPLICATION NUMBER: US/10/340,484
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: 60/347,215
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: 60/353,296
; PRIOR FILING DATE: 2002-02-01
; PRIOR APPLICATION NUMBER: 60/368,955
; PRIOR FILING DATE: 2002-03-28
; PRIOR APPLICATION NUMBER: 60/379,125
; PRIOR FILING DATE: 2002-05-08
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Macaca fascicularis
US-10-340-484-16

Query Match 100.0%; Score 31; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 13
US-10-016-403-5
; Sequence 5, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06
; ATTORNEY/AGENT INFORMATION:
; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "parathyroid hormone"
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-10-016-403-5

Query Match 100.0%; Score 31; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 14

US-10-097-079-1

; Sequence 1, Application US/10097079
; Publication No. US20020132973A1
; GENERAL INFORMATION:
; APPLICANT: Condon, Stephen M.
; Morize, Isabelle
; TITLE OF INVENTION: PEPTIDE PARATHYROID HORMONE ANALOGS
; NUMBER OF SEQUENCES: 88
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rhone-Poulenc Rorer Inc.
; STREET: 500 Arcola Road, Mailstop 3C43
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/097,079
; FILING DATE: 13-Mar-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/228,990
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/046,472
; FILING DATE: 14-MAY-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Martin Esq., Michael B.
; REGISTRATION NUMBER: 37,521
; REFERENCE/DOCKET NUMBER: A2678B-WO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (610) 454-2793
; TELEFAX: (610) 454-3808
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 34 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: No. US20020132973A1 Relevant
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: N-terminal
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:

US-10-097-079-1

Query Match 100.0%; Score 31; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.2e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 15

US-10-168-185-9

; Sequence 9, Application US/10168185
; Publication No. US20030175802A1
; GENERAL INFORMATION:
; APPLICANT: Armbruster, Franz Paul
; APPLICANT: Missbichler, Albert
; APPLICANT: Schmidt-Gayk, Heinrich
; APPLICANT: Roth, Heinz-Jurgen
; TITLE OF INVENTION: Method for Determining Parathormone
; TITLE OF INVENTION: Activity in a Human Sample
; FILE REFERENCE: HLZ-004US
; CURRENT APPLICATION NUMBER: US/10/168,185
; CURRENT FILING DATE: 2002-06-17
; PRIOR APPLICATION NUMBER: PCT/EP00/12911
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: DE 19961350
; PRIOR FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-168-185-9

Query Match 100.0%; Score 31; DB 12; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 16

US-09-169-786-4

; Sequence 4, Application US/09169786B
; Patent No. US20020025929A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Masahiko
; TITLE OF INVENTION: METHOD OF BUILDING AND MAINTAINING BONE
; FILE REFERENCE: X-11480
; CURRENT APPLICATION NUMBER: US/09/169,786B
; CURRENT FILING DATE: 1998-10-09
; EARLIER APPLICATION NUMBER: US 60/061,800
; EARLIER FILING DATE: 1997-10-14
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens

US-09-169-786-4

Query Match 100.0%; Score 31; DB 9; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
||||||||||||||||||||||||||||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 17

US-09-843-221A-14

; Sequence 14, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUJK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-14

Query Match 100.0%; Score 31; DB 11; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
||||||||||||||||||||||||||||||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 18

US-10-245-707-1

; Sequence 1, Application US/10245707
; Publication No. US20030171282A1
; GENERAL INFORMATION:
; APPLICANT: Patton, John S.
; TITLE OF INVENTION: Pulmonary Delivery of Active Fragments of Parathyroid
Hormone
; FILE REFERENCE: 032055-047
; CURRENT APPLICATION NUMBER: US/10/245,707

```
; CURRENT FILING DATE: 2003-03-11
; PRIOR APPLICATION NUMBER: US 09/577,264
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: US 09/128,401
; PRIOR FILING DATE: 1998-08-03
; PRIOR APPLICATION NUMBER: US 08/625,586
; PRIOR FILING DATE: 1996-03-28
; PRIOR APPLICATION NUMBER: US 08/232,849
; PRIOR FILING DATE: 1994-04-25
; PRIOR APPLICATION NUMBER: US 07/953,397
; PRIOR FILING DATE: 1992-09-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 38
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: parathyroid hormone (PTH) fragment molecules
US-10-245-707-1
```

```
Query Match          100.0%; Score 31; DB 12; Length 38;
Best Local Similarity 100.0%; Pred. No. 1.3e-24;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
          |||||
Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
```

RESULT 19

```
US-09-843-221A-39
; Sequence 39, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 39
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-39
```

Query Match 96.8%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 20

US-09-843-221A-166

; Sequence 166, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 166
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (30)..(30)
; OTHER INFORMATION: Optional linker and Fc domain attached at the C-terminus
US-09-843-221A-166

Query Match 96.8%; Score 30; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.1e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 21

US-10-361-928-3

; Sequence 3, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:

```

; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:
;   NAME/KEY: MOD_RES
;   LOCATION: (1)
;   OTHER INFORMATION: Desamino Gly
US-10-361-928-3

```

```

Query Match          96.8%; Score 30; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches    30; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

RESULT 22

US-10-361-928-6

```

; Sequence 6, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
;   LENGTH: 33
;   TYPE: PRT
;   ORGANISM: Homo sapiens
;   FEATURE:

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; NAME/KEY: MOD_RES
; LOCATION: (1)
; OTHER INFORMATION: Desamino Ala
US-10-361-928-6

Query Match 96.8%; Score 30; DB 12; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.2e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 23

US-09-843-221A-20

; Sequence 20, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-20

Query Match 96.8%; Score 30; DB 11; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 24

US-10-361-928-1

; Sequence 1, Application US/10361928
; Publication No. US20030144209A1

```

; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (1)
; OTHER INFORMATION: Can be desamino Ser, desamino Ala, or desamino Gly
US-10-361-928-1

```

```

Query Match          96.8%; Score 30; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.3e-23;
Matches    30; Conservative    0; Mismatches    0; Indels    0; Gaps    0;

```

```

Qy      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        ||||||||||||||||||||||||||||
Db      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

```

```

RESULT 25
US-10-361-928-2
; Sequence 2, Application US/10361928
; Publication No. US20030144209A1
; GENERAL INFORMATION:
; APPLICANT: BRINGHURST, F. RICHARD
; APPLICANT: TAKASU, HISASHI
; APPLICANT: GARDELLA, THOMAS J.
; TITLE OF INVENTION: AMINO-TERMINAL MODIFIED PARATHYROID HORMONE (PTH)
; TITLE OF INVENTION: ANALOGS
; FILE REFERENCE: 0609.4630002
; CURRENT APPLICATION NUMBER: US/10/361,928
; CURRENT FILING DATE: 2003-02-11
; PRIOR APPLICATION NUMBER: 09/447,800
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: 60/110,152
; PRIOR FILING DATE: 1998-11-25
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens

```



```
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-15
```

```
Query Match          96.8%; Score 30; DB 11; Length 37;
Best Local Similarity 100.0%; Pred. No. 1.4e-23;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
Qy      2 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31
        |||
Db      1 VSEIQLMHNLGKHLNSMERVEWLRKKLQDV 30
```

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RESULT 28
US-09-843-221A-51
; Sequence 51, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 51
; LENGTH: 29
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-51

Query Match 93.5%; Score 29; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 29

US-09-843-221A-167

; Sequence 167, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 167
; LENGTH: 29
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
US-09-843-221A-167

Query Match 93.5%; Score 29; DB 11; Length 29;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQ 29

RESULT 30

US-09-843-221A-43
; Sequence 43, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-43

Query Match 93.5%; Score 29; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.2e-22;
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30
|||||
Db 2 VSEIQLMHNLGKHLNSMERVEWLRKKLQD 30

RESULT 31
US-09-843-221A-52
; Sequence 52, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053

; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 52
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-843-221A-52

Query Match 90.3%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 32

US-09-843-221A-168

; Sequence 168, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 168
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Preferred embodiments - PTH
; NAME/KEY: misc_feature
; LOCATION: (1)..(1)
; OTHER INFORMATION: Fc domain attached at the N-terminus through optional
linker
US-09-843-221A-168

Query Match 90.3%; Score 28; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.2e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

Db 1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

RESULT 33

US-10-372-095-24

; Sequence 24, Application US/10372095
; Publication No. US20030162256A1
; GENERAL INFORMATION:
; APPLICANT: Juppner, Harald
; APPLICANT: Rubin, David A.
; TITLE OF INVENTION: PTH1R and PTH3R Receptors, Methods and Uses Thereof
; FILE REFERENCE: 0609.4740002
; CURRENT APPLICATION NUMBER: US/10/372,095
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/449,632
; PRIOR FILING DATE: 1999-11-30
; PRIOR APPLICATION NUMBER: US 60/110,467
; PRIOR FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 34
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-372-095-24

Query Match 90.3%; Score 28; DB 12; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQLMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 4 EIQLMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 34

US-10-016-403-7

; Sequence 7, Application US/10016403
; Publication No. US20020107505A1
; GENERAL INFORMATION:
; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

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;      CURRENT APPLICATION DATA:
;      APPLICATION NUMBER: US/10/016,403
;      FILING DATE: 10-Dec-2001
;      CLASSIFICATION: <Unknown>
;      PRIOR APPLICATION DATA:
;      APPLICATION NUMBER: 08/466,610
;      FILING DATE: 1995-JUN-06
;      ATTORNEY/AGENT INFORMATION:
;      NAME: Frenchick, Grady J.
;      REGISTRATION NUMBER: 29,018
;      REFERENCE/DOCKET NUMBER: 8734.28
;      TELECOMMUNICATION INFORMATION:
;      TELEPHONE: 608-257-2281
;      TELEFAX: 608-257-7643
;      INFORMATION FOR SEQ ID NO: 7:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH: 34 amino acids
;      TYPE: amino acid
;      TOPOLOGY: linear
;      FEATURE:
;      NAME/KEY: Peptide
;      LOCATION: 1..34
;      OTHER INFORMATION: /note= "modified parathyroid
;      hormone"
;      SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-016-403-7

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Query Match          90.3%; Score 28; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.4e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28
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Db      1 SVSEIQLMHNLGKHLNSMERVEWLRKKL 28

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RESULT 35
US-09-843-221A-50
; Sequence 50, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170

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; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 50
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-50

Query Match 83.9%; Score 26; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.3e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 36

US-09-843-221A-28
; Sequence 28, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 28
; LENGTH: 31
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-28

Query Match 83.9%; Score 26; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 1.4e-19;
Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
|||
Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 37

US-10-031-874A-206

; Sequence 206, Application US/10031874A
 ; Publication No. US20030190598A1
 ; GENERAL INFORMATION:
 ; APPLICANT: TANHA, JAMSHID
 ; APPLICANT: DUBUC, GINETTE
 ; APPLICANT: NARANG, SARAN
 ; TITLE OF INVENTION: SINGLE-DOMAIN ANTIGEN-BINDING ANTIBODY FRAGMENTS
 ; TITLE OF INVENTION: DERIVED FROM LLAMA ANTIBODIES
 ; FILE REFERENCE: 11054-1
 ; CURRENT APPLICATION NUMBER: US/10/031,874A
 ; CURRENT FILING DATE: 2002-11-14
 ; PRIOR APPLICATION NUMBER: 60/207,234
 ; PRIOR FILING DATE: 2000-05-26
 ; NUMBER OF SEQ ID NOS: 212
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 206
 ; LENGTH: 31
 ; TYPE: PRT
 ; ORGANISM: Lama glama
 US-10-031-874A-206

Query Match 83.9%; Score 26; DB 12; Length 31;
 Best Local Similarity 100.0%; Pred. No. 1.4e-19;
 Matches 26; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26
 |||||
 Db 1 SVSEIQLMHNLGKHLNSMERVEWLRK 26

RESULT 38

US-09-843-221A-32

; Sequence 32, Application US/09843221A
 ; Publication No. US20030039654A1
 ; GENERAL INFORMATION:
 ; APPLICANT: KOSTENUIK, PAUL
 ; APPLICANT: LIU, CHUAN-FA
 ; APPLICANT: LACEY, DAVID LEE
 ; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
 PARATHYROID HORMONE-
 ; TITLE OF INVENTION: RELATED PROTEIN
 ; FILE REFERENCE: A-665B
 ; CURRENT APPLICATION NUMBER: US/09/843,221A
 ; CURRENT FILING DATE: 2001-04-26
 ; PRIOR APPLICATION NUMBER: 60/266,673
 ; PRIOR FILING DATE: 2001-02-06
 ; PRIOR APPLICATION NUMBER: 60/214,860
 ; PRIOR FILING DATE: 2000-06-28
 ; PRIOR APPLICATION NUMBER: 60/200,053
 ; PRIOR FILING DATE: 2000-04-27
 ; NUMBER OF SEQ ID NOS: 170
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 32
 ; LENGTH: 28
 ; TYPE: PRT

; ORGANISM: Homo sapiens
US-09-843-221A-32

Query Match 80.6%; Score 25; DB 11; Length 28;
Best Local Similarity 100.0%; Pred. No. 1.3e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHNLGKHLNSMERVEWLRKKLQDV 31
|||||
Db 1 LMHNLGKHLNSMERVEWLRKKLQDV 25

RESULT 39

US-10-016-403-6

; Sequence 6, Application US/10016403
; Publication No. US20020107505A1

; GENERAL INFORMATION:

; APPLICANT: Holladay, Leslie A.
; TITLE OF INVENTION: MODIFICATION OF POLYPEPTIDE DRUGS TO
; INCREASE ELECTROTRANSPORT FLUX
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Stroud, Stroud, Willink, Thompson & Howard
; STREET: 25 West Main Street
; CITY: Madison
; STATE: WI
; COUNTRY: USA
; ZIP: 53701-2236

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/10/016,403
; FILING DATE: 10-Dec-2001
; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/466,610
; FILING DATE: 1995-JUN-06

; ATTORNEY/AGENT INFORMATION:

; NAME: Frenchick, Grady J.
; REGISTRATION NUMBER: 29,018
; REFERENCE/DOCKET NUMBER: 8734.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 608-257-2281
; TELEFAX: 608-257-7643

; INFORMATION FOR SEQ ID NO: 6:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 34 amino acids
; TYPE: amino acid
; TOPOLOGY: linear

; FEATURE:

; NAME/KEY: Peptide
; LOCATION: 1..34
; OTHER INFORMATION: /note= "modified parathyroid
; hormone"

; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-016-403-6

Query Match 80.6%; Score 25; DB 14; Length 34;
Best Local Similarity 100.0%; Pred. No. 1.5e-18;
Matches 25; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 LMHNLGKHLNSMERVEWLRKKLQDV 31
||||||||||||||||
Db 7 LMHNLGKHLNSMERVEWLRKKLQDV 31

RESULT 40

US-09-843-221A-124

; Sequence 124, Application US/09843221A
; Publication No. US20030039654A1
; GENERAL INFORMATION:
; APPLICANT: KOSTENUIK, PAUL
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: LACEY, DAVID LEE
; TITLE OF INVENTION: MODULATORS OF RECEPTORS FOR PARATHYROID HORMONE AND
PARATHYROID HORMONE-
; TITLE OF INVENTION: RELATED PROTEIN
; FILE REFERENCE: A-665B
; CURRENT APPLICATION NUMBER: US/09/843,221A
; CURRENT FILING DATE: 2001-04-26
; PRIOR APPLICATION NUMBER: 60/266,673
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: 60/214,860
; PRIOR FILING DATE: 2000-06-28
; PRIOR APPLICATION NUMBER: 60/200,053
; PRIOR FILING DATE: 2000-04-27
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 124
; LENGTH: 30
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified human PTH
US-09-843-221A-124

Query Match 71.0%; Score 22; DB 11; Length 30;
Best Local Similarity 100.0%; Pred. No. 1.6e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEIQLMHNLGKHLNSMERVE 22
||||||||||||||||
Db 1 SVSEIQLMHNLGKHLNSMERVE 22

Search completed: January 14, 2004, 11:15:07
Job time : 21.8598 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 23.1776 Seconds
(without alignments)
345.145 Million cell updates/sec

Title: US-09-843-221A-165
Perfect score: 31
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size : 0

Total number of hits satisfying chosen parameters: 13497

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SPTREMBL_23:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
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10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp Vertebrate:*
14: sp_unclassified:*
15: sp_rvirus:*
16: sp_bacteriap:*
17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	%	Query					
No.	Score	Match	Length	DB	ID		Description

1	14	45.2	31	11	Q91Y90	Q91y90 peromyscus
2	14	45.2	31	11	Q91Y91	Q91y91 peromyscus
3	5	16.1	34	5	O17148	O17148 echinococcu
4	5	16.1	34	16	Q97K50	Q97k50 clostridium
5	5	16.1	34	17	Q9HR65	Q9hr65 halobacteri
6	5	16.1	35	11	Q8BTB9	Q8btb9 mus musculu
7	5	16.1	35	16	Q97RG6	Q97rg6 streptococc
8	4	12.9	28	10	O24285	O24285 pinus radia
9	4	12.9	28	10	Q8GZQ8	Q8gzz8 hordeum vul
10	4	12.9	29	2	Q49148	Q49148 methylobact
11	4	12.9	29	4	Q9UCL2	Q9ucl2 homo sapien
12	4	12.9	29	4	Q96PP3	Q96pp3 homo sapien
13	4	12.9	29	5	Q25603	Q25603 onchocerca
14	4	12.9	29	13	O13043	O13043 scyliorhinu
15	4	12.9	30	2	Q9JMV3	Q9jmv3 escherichia
16	4	12.9	30	4	Q9UBV5	Q9ubv5 homo sapien
17	4	12.9	30	16	Q8DZP7	Q8dzz7 streptococc
18	4	12.9	31	1	Q55314	Q55314 sulfolobus
19	4	12.9	31	4	Q8NEI8	Q8nei8 homo sapien
20	4	12.9	31	8	Q9MS77	Q9ms77 phacus acum
21	4	12.9	31	16	O50669	O50669 borrelia bu
22	4	12.9	32	11	Q9QZQ2	Q9qzz2 mus musculu
23	4	12.9	32	17	Q9HSZ0	Q9hsz0 halobacteri
24	4	12.9	33	5	Q95SD4	Q95sd4 drosophila
25	4	12.9	33	16	Q9PKX3	Q9pkx3 chlamydia m
26	4	12.9	34	2	Q9ZG81	Q9zgz81 chlamydia t
27	4	12.9	34	2	Q8GFK2	Q8gfk2 staphylococ
28	4	12.9	34	11	Q8C4P4	Q8c4p4 mus musculu
29	4	12.9	34	13	Q90ZJ4	Q90zz4 gallus gall
30	4	12.9	34	16	Q98FK5	Q98fk5 rhizobium l
31	4	12.9	34	16	Q8G2Q2	Q8g2q2 brucella su
32	4	12.9	35	4	Q15421	Q15421 homo sapien
33	4	12.9	35	12	Q8V6J8	Q8v6j8 halovirus h
34	4	12.9	35	16	Q9KQG4	Q9kqg4 vibrio chol
35	4	12.9	35	16	Q8F102	Q8f102 leptospira
36	4	12.9	36	2	Q53920	Q53920 streptomyce
37	4	12.9	36	2	O68941	O68941 rhodospiril
38	4	12.9	36	4	Q8WXW8	Q8wxw8 homo sapien
39	4	12.9	36	10	Q9SJ63	Q9sj63 arabidopsis
40	4	12.9	36	12	Q9PXD1	Q9pxd1 hepatitis c
41	4	12.9	36	12	Q91D77	Q91d77 ttv-like mi
42	4	12.9	36	13	Q9YHT9	Q9yht9 brachydanio
43	4	12.9	36	16	Q97S91	Q97s91 streptococc
44	4	12.9	37	2	Q8KYJ0	Q8kyj0 bacillus an
45	4	12.9	37	5	Q9N2L2	Q9n2l2 caenorhabdi
46	4	12.9	37	10	Q39942	Q39942 helianthus
47	4	12.9	37	13	Q8AWW8	Q8aww8 oncorhynchu
48	4	12.9	37	16	Q8F6U2	Q8f6u2 leptospira
49	4	12.9	37	16	Q8F5H3	Q8f5h3 leptospira
50	4	12.9	37	16	Q8F419	Q8f419 leptospira
51	4	12.9	37	16	Q8EXV9	Q8exv9 leptospira
52	4	12.9	38	2	Q8KWH7	Q8kwh7 lactobacill
53	4	12.9	38	5	Q9NBE3	Q9nbe3 chironomus
54	4	12.9	38	5	Q9NBE5	Q9nbe5 chironomus
55	4	12.9	38	5	Q9NBE8	Q9nbe8 chironomus
56	4	12.9	38	5	Q9NBE4	Q9nbe4 chironomus
57	4	12.9	38	5	Q9NBE7	Q9nbe7 chironomus

58	4	12.9	38	11	Q91VC8	Q91vc8 mus musculu
59	4	12.9	38	13	Q8AWW9	Q8aww9 oncorhynchu
60	4	12.9	38	16	Q8E0D2	Q8e0d2 streptococc
61	4	12.9	39	2	Q8GPQ8	Q8gppq8 pseudomonas
62	4	12.9	39	10	Q9FEY1	Q9fey1 heterocapsa
63	4	12.9	39	12	Q68847	Q68847 hepatitis c
64	4	12.9	39	12	Q68845	Q68845 hepatitis c
65	4	12.9	39	12	Q68846	Q68846 hepatitis c
66	4	12.9	39	13	Q90776	Q90776 gallus gall
67	4	12.9	39	16	Q9KYH4	Q9kyh4 streptomyce
68	4	12.9	39	16	Q8F0C7	Q8f0c7 leptospira
69	4	12.9	39	16	Q8EZ33	Q8ez33 leptospira
70	4	12.9	40	2	Q8GCS7	Q8gcs7 eubacterium
71	4	12.9	40	4	P78340	P78340 homo sapien
72	4	12.9	40	6	Q29283	Q29283 sus scrofa
73	4	12.9	40	10	Q8H192	Q8h192 arabidopsis
74	4	12.9	40	12	Q91JZ7	Q91jz7 hepatitis c
75	4	12.9	40	12	Q8V647	Q8v647 rabies viru
76	3	9.7	28	2	Q01303	Q01303 treponema p
77	3	9.7	28	2	Q05574	Q05574 prochloroth
78	3	9.7	28	2	Q9ZB83	Q9zb83 vibrio angu
79	3	9.7	28	3	Q8TGT8	Q8tgt8 saccharomyc
80	3	9.7	28	4	Q96SD9	Q96sd9 homo sapien
81	3	9.7	28	4	Q16326	Q16326 homo sapien
82	3	9.7	28	4	Q96EU0	Q96eu0 homo sapien
83	3	9.7	28	4	O75980	O75980 homo sapien
84	3	9.7	28	4	O95737	O95737 homo sapien
85	3	9.7	28	5	Q8MUW0	Q8muw0 schistosoma
86	3	9.7	28	5	Q8MPY2	Q8mpy2 caenorhabdi
87	3	9.7	28	5	Q9BM68	Q9bm68 glottidia p
88	3	9.7	28	5	Q9BJE4	Q9bje4 pauropus sp
89	3	9.7	28	6	O62821	O62821 bubalus bub
90	3	9.7	28	6	Q9XS89	Q9xs89 equus cabal
91	3	9.7	28	8	Q8WBC8	Q8wbc8 cucurbita e
92	3	9.7	28	8	Q9TIE9	Q9tie9 centella er
93	3	9.7	28	8	Q9TIE8	Q9tie8 centella as
94	3	9.7	28	8	Q9MR96	Q9mr96 crocodylus
95	3	9.7	28	8	Q9TIE6	Q9tie6 centella hi
96	3	9.7	28	8	Q9ZYS4	Q9zys4 leishmania
97	3	9.7	28	8	Q9MR94	Q9mr94 chelonias my
98	3	9.7	28	8	Q9TIE7	Q9tie7 centella tr
99	3	9.7	28	8	Q8HS23	Q8hs23 pisum sativ
100	3	9.7	28	8	Q8HS11	Q8hs11 spathiphyll
101	3	9.7	28	8	Q8HS07	Q8hs07 welwitschia
102	3	9.7	28	8	Q8HKF0	Q8hkf0 rhipicephal
103	3	9.7	28	9	Q9AZJ9	Q9azj9 bacterioph
104	3	9.7	28	9	Q38269	Q38269 bacterioph
105	3	9.7	28	10	Q8S526	Q8s526 ipomoea bat
106	3	9.7	28	10	Q8W232	Q8w232 zea mays (m
107	3	9.7	28	10	Q944P1	Q944p1 manihot esc
108	3	9.7	28	11	Q9ESI4	Q9esi4 petromus ty
109	3	9.7	28	11	Q9ESI5	Q9esi5 thryonomys
110	3	9.7	28	11	Q9ESI6	Q9esi6 hystrich afr
111	3	9.7	28	11	Q99PL9	Q99pl9 mus musculu
112	3	9.7	28	11	Q9ESI2	Q9esi2 cryptomys h
113	3	9.7	28	11	Q9EP60	Q9ep60 heliophobi
114	3	9.7	28	11	Q9ESI0	Q9esi0 cryptomys s

115	3	9.7	28	11	Q91XP0	Q91xp0 rattus norv
116	3	9.7	28	11	P70651	P70651 mus sp. bet
117	3	9.7	28	11	Q9EP59	Q9ep59 georychus c
118	3	9.7	28	11	Q9ESI1	Q9esi1 cryptomys d
119	3	9.7	28	11	P97914	P97914 rattus norv
120	3	9.7	28	11	Q9EP61	Q9ep61 heteroceph
121	3	9.7	28	11	Q9ESH8	Q9esh8 bathyergus
122	3	9.7	28	11	Q9ESH9	Q9esh9 bathyergus
123	3	9.7	28	11	Q9QXB4	Q9qxb4 mus musculu
124	3	9.7	28	11	Q9ESI3	Q9esi3 cryptomys h
125	3	9.7	28	12	Q68087	Q68087 hepatitis c
126	3	9.7	28	12	Q67786	Q67786 human adeno
127	3	9.7	28	12	Q68095	Q68095 hepatitis c
128	3	9.7	28	12	Q68097	Q68097 hepatitis c
129	3	9.7	28	12	Q68092	Q68092 hepatitis c
130	3	9.7	28	12	Q68091	Q68091 hepatitis c
131	3	9.7	28	12	Q68093	Q68093 hepatitis c
132	3	9.7	28	12	Q68099	Q68099 hepatitis c
133	3	9.7	28	12	Q68096	Q68096 hepatitis c
134	3	9.7	28	12	Q68098	Q68098 hepatitis c
135	3	9.7	28	12	Q83181	Q83181 cauliflower
136	3	9.7	28	12	Q68086	Q68086 hepatitis c
137	3	9.7	28	12	Q68552	Q68552 hepatitis c
138	3	9.7	28	12	Q68094	Q68094 hepatitis c
139	3	9.7	28	12	Q9WNI4	Q9wni4 tt virus. o
140	3	9.7	28	13	Q9PRE8	Q9pre8 oryzias lat
141	3	9.7	28	13	Q9PRI9	Q9pri9 amia calva
142	3	9.7	28	13	Q9PRN8	Q9prn8 carassius a
143	3	9.7	28	15	O71346	O71346 human endog
144	3	9.7	28	15	Q9QEY3	Q9qey3 human immun
145	3	9.7	28	16	Q8X415	Q8x415 escherichia
146	3	9.7	28	16	Q8NVB8	Q8nvb8 staphylococ
147	3	9.7	28	16	Q8ENT7	Q8ent7 oceanobacil
148	3	9.7	28	16	Q8CK95	Q8ck95 yersinia pe
149	3	9.7	29	2	Q9ZGG4	Q9zgg4 heliobacill
150	3	9.7	29	2	Q54200	Q54200 streptomyce
151	3	9.7	29	2	Q9X3E3	Q9x3e3 prochloroco
152	3	9.7	29	2	Q9X3J9	Q9x3j9 prochloroco
153	3	9.7	29	2	Q47650	Q47650 escherichia
154	3	9.7	29	2	Q9AKV1	Q9akv1 neisseria g
155	3	9.7	29	2	Q9R526	Q9r526 vibrio chol
156	3	9.7	29	3	P78747	P78747 saccharomyc
157	3	9.7	29	3	Q8TGQ5	Q8tgq5 saccharomyc
158	3	9.7	29	4	Q9Y3G1	Q9y3g1 homo sapien
159	3	9.7	29	4	Q9H2A1	Q9h2a1 homo sapien
160	3	9.7	29	4	Q9UN87	Q9un87 homo sapien
161	3	9.7	29	4	Q9H465	Q9h465 homo sapien
162	3	9.7	29	4	Q8NEF6	Q8nef6 homo sapien
163	3	9.7	29	4	Q8TDW8	Q8tdw8 homo sapien
164	3	9.7	29	4	Q96IR5	Q96ir5 homo sapien
165	3	9.7	29	4	Q9BSQ3	Q9bsq3 homo sapien
166	3	9.7	29	5	Q95VB2	Q95vb2 spirometra
167	3	9.7	29	5	Q95NF4	Q95nf4 drosophila
168	3	9.7	29	5	Q8T936	Q8t936 folsomia ca
169	3	9.7	29	6	Q9TRG5	Q9trg5 sus scrofa
170	3	9.7	29	8	Q8WBB9	Q8wbb9 cucurbita f
171	3	9.7	29	8	Q8W7W7	Q8w7w7 cucurbita p

172	3	9.7	29	8	Q9GF70	Q9gf70 trochodendr
173	3	9.7	29	8	Q8W7W4	Q8w7w4 cucurbita a
174	3	9.7	29	8	Q8W7W6	Q8w7w6 cucurbita p
175	3	9.7	29	8	Q8WBC1	Q8wbc1 cucurbita o
176	3	9.7	29	8	Q9B5Z6	Q9b5z6 pseudostylo
177	3	9.7	29	8	Q8W7W5	Q8w7w5 cucurbita p
178	3	9.7	29	8	Q9B938	Q9b938 eupristina
179	3	9.7	29	8	Q9G370	Q9g370 draco blanf
180	3	9.7	29	8	Q8WBD0	Q8wbd0 cucurbita a
181	3	9.7	29	8	Q8WBB6	Q8wbb6 citrullus l
182	3	9.7	29	8	Q8W7W9	Q8w7w9 cucurbita f
183	3	9.7	29	8	Q8W7W8	Q8w7w8 cucurbita m
184	3	9.7	29	8	Q8HS21	Q8hs21 rheum x cul
185	3	9.7	29	9	Q9FZX6	Q9fzx6 bacterioph
186	3	9.7	29	10	P82196	P82196 spinacia ol
187	3	9.7	29	11	Q9Z2C0	Q9z2c0 mus musculu
188	3	9.7	29	11	Q921Z6	Q921z6 mus musculu
189	3	9.7	29	11	Q9Z2C1	Q9z2c1 mus musculu
190	3	9.7	29	11	O70564	O70564 mus musculu
191	3	9.7	29	11	Q9QY65	Q9qy65 mus musculu
192	3	9.7	29	11	Q62300	Q62300 mus musculu
193	3	9.7	29	11	O08980	O08980 mus musculu
194	3	9.7	29	11	Q8CGM8	Q8cgm8 mus musculu
195	3	9.7	29	12	Q91HB1	Q91hb1 porcine cir
196	3	9.7	29	12	O92646	O92646 hepatitis e
197	3	9.7	29	12	Q919A5	Q919a5 porcine rep
198	3	9.7	29	12	Q919A7	Q919a7 porcine rep
199	3	9.7	29	12	Q86872	Q86872 cauliflower
200	3	9.7	29	12	O92648	O92648 hepatitis e
201	3	9.7	29	12	O56835	O56835 vibrio chol
202	3	9.7	29	13	P82235	P82235 rana tempor
203	3	9.7	29	13	Q8AYR0	Q8ayr0 oryzias lat
204	3	9.7	29	13	Q8AWC2	Q8awc2 gallus gall
205	3	9.7	29	15	O72001	O72001 human endog
206	3	9.7	29	15	O71342	O71342 human endog
207	3	9.7	29	15	O71339	O71339 human endog
208	3	9.7	29	15	O71347	O71347 human endog
209	3	9.7	29	15	O71340	O71340 human endog
210	3	9.7	29	15	O71343	O71343 human endog
211	3	9.7	29	15	Q9IQJ8	Q9iqj8 human immun
212	3	9.7	29	15	O71991	O71991 human endog
213	3	9.7	29	15	Q9IQJ1	Q9iqj1 human immun
214	3	9.7	29	15	O71994	O71994 human endog
215	3	9.7	29	15	O71341	O71341 human endog
216	3	9.7	29	15	O71345	O71345 human endog
217	3	9.7	29	15	O71336	O71336 human endog
218	3	9.7	29	15	O71344	O71344 human endog
219	3	9.7	29	15	O71338	O71338 human endog
220	3	9.7	29	15	O71992	O71992 human endog
221	3	9.7	29	15	O71337	O71337 human endog
222	3	9.7	29	15	Q9IQJ9	Q9iqj9 human immun
223	3	9.7	29	15	O71997	O71997 human endog
224	3	9.7	29	15	O71335	O71335 human endog
225	3	9.7	29	16	Q9JZN6	Q9jzn6 neisseria m
226	3	9.7	29	16	Q8X419	Q8x419 escherichia
227	3	9.7	30	2	Q9JP75	Q9jp75 salmonella
228	3	9.7	30	2	Q9L8W9	Q9l8w9 streptomyce

229	3	9.7	30	2	Q9L8X1	Q9l8x1 streptomyce
230	3	9.7	30	2	Q9R4Z6	Q9r4z6 clostridium
231	3	9.7	30	2	Q9REI5	Q9rei5 acidiphiliu
232	3	9.7	30	2	Q9R4J2	Q9r4j2 helicobacte
233	3	9.7	30	2	Q8VUW9	Q8vuw9 staphylococ
234	3	9.7	30	2	Q9R4I5	Q9r4i5 mycoplasma
235	3	9.7	30	2	Q9R5Q3	Q9r5q3 leuconostoc
236	3	9.7	30	2	Q93GF6	Q93gf6 staphylococ
237	3	9.7	30	2	Q45966	Q45966 coxiella bu
238	3	9.7	30	2	Q9R5C4	Q9r5c4 comamonas.
239	3	9.7	30	2	Q9R5K3	Q9r5k3 leptospira
240	3	9.7	30	2	Q9R4I6	Q9r4i6 mycoplasma
241	3	9.7	30	2	Q9RER6	Q9rer6 enterobacte
242	3	9.7	30	3	Q8TGM3	Q8tgm3 saccharomyc
243	3	9.7	30	3	Q9URB0	Q9urb0 candida alb
244	3	9.7	30	3	Q8J172	Q8j172 trichoderma
245	3	9.7	30	3	Q8J171	Q8j171 hypocrea li
246	3	9.7	30	4	Q16330	Q16330 homo sapien
247	3	9.7	30	4	O95595	O95595 homo sapien
248	3	9.7	30	4	P78460	P78460 homo sapien
249	3	9.7	30	4	Q8N563	Q8n563 homo sapien
250	3	9.7	30	4	P78542	P78542 homo sapien
251	3	9.7	30	4	Q8IU66	Q8iu66 homo sapien
252	3	9.7	30	5	Q8SZJ6	Q8szj6 drosophila
253	3	9.7	30	5	Q9TWH7	Q9twh7 ancylostoma
254	3	9.7	30	5	Q968N1	Q968n1 tritrichomo
255	3	9.7	30	5	P82214	P82214 bombyx mori
256	3	9.7	30	6	Q9BDK1	Q9bdk1 bos taurus
257	3	9.7	30	6	Q9TTF9	Q9ttf9 ateles belz
258	3	9.7	30	8	Q8W7L1	Q8w7l1 cucurbita m
259	3	9.7	30	8	Q8W7K9	Q8w7k9 cucurbita p
260	3	9.7	30	8	Q8W7H8	Q8w7h8 cucurbita a
261	3	9.7	30	8	Q8WBC2	Q8wbc2 cucurbita o
262	3	9.7	30	8	Q8W7K8	Q8w7k8 cucurbita p
263	3	9.7	30	8	Q8W7H6	Q8w7h6 cucurbita m
264	3	9.7	30	8	Q8WBC4	Q8wbc4 cucurbita p
265	3	9.7	30	8	Q8W7L2	Q8w7l2 cucurbita a
266	3	9.7	30	8	Q8WBC6	Q8wbc6 cucurbita a
267	3	9.7	30	8	Q8WBB7	Q8wbb7 sechium edu
268	3	9.7	30	8	Q99328	Q99328 meloidogyne
269	3	9.7	30	8	Q8W7H7	Q8w7h7 cucurbita e
270	3	9.7	30	8	Q8WBC0	Q8wbc0 cucurbita f
271	3	9.7	30	8	Q9T2T8	Q9t2t8 bos taurus
272	3	9.7	30	8	Q8W7L0	Q8w7l0 cucurbita p
273	3	9.7	30	8	Q8HKG1	Q8hkg1 rhipicephal
274	3	9.7	30	9	Q8W674	Q8w674 enterobacte
275	3	9.7	30	10	Q9S8T2	Q9s8t2 cicer ariet
276	3	9.7	30	10	O23933	O23933 flaveria tr
277	3	9.7	30	10	Q8RUD1	Q8rud1 zea mays (m
278	3	9.7	30	10	Q93WY2	Q93wy2 oryza sativ
279	3	9.7	30	11	Q63885	Q63885 mus sp. cys
280	3	9.7	30	11	O88549	O88549 mesocricetu
281	3	9.7	30	11	Q8VDL1	Q8vdl1 mus musculu
282	3	9.7	30	11	Q9QV18	Q9qv18 rattus sp.
283	3	9.7	30	11	Q9QV14	Q9qv14 mus sp. col
284	3	9.7	30	11	Q9QV19	Q9qv19 rattus sp.
285	3	9.7	30	11	Q10753	Q10753 rattus norv

286	3	9.7	30	11	Q8BR32	Q8br32 mus musculu
287	3	9.7	30	12	Q91HB7	Q91hb7 tt virus. o
288	3	9.7	30	12	Q91HC4	Q91hc4 tt virus. o
289	3	9.7	30	12	Q9IJV5	Q9ijv5 norwalk vir
290	3	9.7	30	12	Q86870	Q86870 cauliflower
291	3	9.7	30	12	Q91HC3	Q91hc3 tt virus. o
292	3	9.7	30	12	Q9WLK3	Q9wlk3 hepatitis e
293	3	9.7	30	12	Q91HC0	Q91hc0 tt virus. o
294	3	9.7	30	13	O42551	O42551 brachydanio
295	3	9.7	30	13	Q9PRW0	Q9prw0 struthio ca
296	3	9.7	30	13	Q9PT00	Q9pt00 oncorhynch
297	3	9.7	30	15	Q86599	Q86599 human endog
298	3	9.7	30	15	Q991P5	Q991p5 human immun
299	3	9.7	30	16	O50822	O50822 borrelia bu
300	3	9.7	30	16	Q9X0W9	Q9x0w9 thermotoga
301	3	9.7	30	16	Q9PP53	Q9pp53 campylobact
302	3	9.7	30	16	Q9KU55	Q9ku55 vibrio chol
303	3	9.7	30	16	Q9JWF4	Q9jwf4 neisseria m
304	3	9.7	30	16	Q97SX5	Q97sx5 streptococc
305	3	9.7	30	16	Q9K1W7	Q9k1w7 chlamydia p
306	3	9.7	30	16	Q8U566	Q8u566 agrobacteri
307	3	9.7	30	16	Q8KE55	Q8ke55 chlorobium
308	3	9.7	30	16	Q93RS7	Q93rs7 streptomyce
309	3	9.7	30	16	Q8G1R1	Q8glr1 brucella su
310	3	9.7	30	16	Q8FZX9	Q8fzx9 brucella su
311	3	9.7	30	16	Q8CU88	Q8cu88 staphylococ
312	3	9.7	30	17	Q8ZZF0	Q8zzf0 pyrobaculum
313	3	9.7	30	17	Q8ZVL0	Q8zvl0 pyrobaculum
314	3	9.7	31	2	Q9S619	Q9s619 prochloroco
315	3	9.7	31	2	Q8KYK0	Q8kyk0 bacillus an
316	3	9.7	31	2	Q9JMV2	Q9jmv2 escherichia
317	3	9.7	31	2	Q9X3C3	Q9x3c3 prochloroco
318	3	9.7	31	2	O68825	O68825 pseudomonas
319	3	9.7	31	2	Q9KH08	Q9kh08 thermus aqu
320	3	9.7	31	2	Q93GF7	Q93gf7 staphylococ
321	3	9.7	31	2	Q47323	Q47323 escherichia
322	3	9.7	31	2	Q9RHF9	Q9rhf9 acinetobact
323	3	9.7	31	2	Q9R4X1	Q9r4x1 treponema d
324	3	9.7	31	2	Q8KYI9	Q8kyi9 bacillus an
325	3	9.7	31	2	Q8RTS5	Q8rts5 uncultured
326	3	9.7	31	2	Q8L3D3	Q8l3d3 colwellia m
327	3	9.7	31	3	O94120	O94120 saccharomyc
328	3	9.7	31	4	Q96A45	Q96a45 homo sapien
329	3	9.7	31	4	Q9UHM9	Q9uhm9 homo sapien
330	3	9.7	31	4	Q9UEA9	Q9uea9 homo sapien
331	3	9.7	31	4	Q8WYF5	Q8wyf5 homo sapien
332	3	9.7	31	4	Q8N5X3	Q8n5x3 homo sapien
333	3	9.7	31	4	Q9BXM4	Q9bxm4 homo sapien
334	3	9.7	31	4	Q9UDE5	Q9ude5 homo sapien
335	3	9.7	31	5	Q8IQV3	Q8iqv3 drosophila
336	3	9.7	31	5	Q8IEY3	Q8iey3 trypanosoma
337	3	9.7	31	6	Q8MI94	Q8mi94 tupaia tana
338	3	9.7	31	6	Q9GLD6	Q9gld6 sus scrofa
339	3	9.7	31	6	Q8MIH5	Q8mih5 canis famil
340	3	9.7	31	6	O77625	O77625 bos taurus
341	3	9.7	31	6	Q8MIC3	Q8mic3 ochotona pr
342	3	9.7	31	6	Q95LC0	Q95lc0 sus scrofa

343	3	9.7	31	6	Q9N1C8	Q9n1c8	ovis aries
344	3	9.7	31	6	Q8MIC9	Q8mic9	nycticebus
345	3	9.7	31	6	Q9GKL4	Q9gkl4	canis famil
346	3	9.7	31	6	Q8MIG4	Q8mig4	cynocephalu
347	3	9.7	31	6	Q9XSB9	Q9xsb9	ateles belz
348	3	9.7	31	7	Q29868	Q29868	homo sapien
349	3	9.7	31	8	Q9MNM2	Q9mnm2	bufo americ
350	3	9.7	31	8	Q9MS59	Q9ms59	euglena san
351	3	9.7	31	8	O80011	O80011	enallagma a
352	3	9.7	31	8	Q9MS62	Q9ms62	euglena myx
353	3	9.7	31	8	Q34922	Q34922	limulus pol
354	3	9.7	31	8	Q8WEJ4	Q8wej4	gnetum gnem
355	3	9.7	31	8	Q9MS74	Q9ms74	euglena ana
356	3	9.7	31	8	Q9MS68	Q9ms68	euglena des
357	3	9.7	31	8	Q8M9Y3	Q8m9y3	chaetosphae
358	3	9.7	31	8	Q9MS53	Q9ms53	euglena vir
359	3	9.7	31	8	Q9MNL2	Q9mnl2	torrentophr
360	3	9.7	31	8	Q9MS56	Q9ms56	euglena ste
361	3	9.7	31	8	Q9MS78	Q9ms78	phacus acum
362	3	9.7	31	8	Q9MNL3	Q9mnl3	torrentophr
363	3	9.7	31	9	Q38499	Q38499	bacterioph
364	3	9.7	31	10	Q9XIT0	Q9xit0	glycine max
365	3	9.7	31	10	Q8LKB4	Q8lkb4	musa acumin
366	3	9.7	31	11	Q8K1W2	Q8klw2	cavia porce
367	3	9.7	31	11	Q9QXB6	Q9qxb6	mus musculu
368	3	9.7	31	11	Q99KK6	Q99kk6	mus musculu
369	3	9.7	31	11	Q8K1P4	Q8klp4	sciurus vul
370	3	9.7	31	11	Q8CGM7	Q8cgm7	mus musculu
371	3	9.7	31	12	Q919E5	Q919e5	human papil
372	3	9.7	31	12	Q919E4	Q919e4	human papil
373	3	9.7	31	12	O56713	O56713	hepatitis c
374	3	9.7	31	12	Q919F7	Q919f7	human papil
375	3	9.7	31	12	Q919E6	Q919e6	human papil
376	3	9.7	31	12	O56692	O56692	hepatitis c
377	3	9.7	31	12	Q919F3	Q919f3	human papil
378	3	9.7	31	12	O56707	O56707	hepatitis c
379	3	9.7	31	12	O56687	O56687	hepatitis c
380	3	9.7	31	12	Q919F8	Q919f8	human papil
381	3	9.7	31	12	O56691	O56691	hepatitis c
382	3	9.7	31	12	Q919E1	Q919e1	human papil
383	3	9.7	31	12	O56701	O56701	hepatitis c
384	3	9.7	31	12	O56694	O56694	hepatitis c
385	3	9.7	31	12	Q919D9	Q919d9	human papil
386	3	9.7	31	12	Q919F6	Q919f6	human papil
387	3	9.7	31	12	Q919E3	Q919e3	human papil
388	3	9.7	31	12	O56712	O56712	hepatitis c
389	3	9.7	31	12	Q919E8	Q919e8	human papil
390	3	9.7	31	12	O56710	O56710	hepatitis c
391	3	9.7	31	12	O56688	O56688	hepatitis c
392	3	9.7	31	12	O56696	O56696	hepatitis c
393	3	9.7	31	12	O56695	O56695	hepatitis c
394	3	9.7	31	12	O56698	O56698	hepatitis c
395	3	9.7	31	12	O56702	O56702	hepatitis c
396	3	9.7	31	12	O56703	O56703	hepatitis c
397	3	9.7	31	12	O56697	O56697	hepatitis c
398	3	9.7	31	12	Q919F0	Q919f0	human papil
399	3	9.7	31	12	O56709	O56709	hepatitis c

400	3	9.7	31	12	Q919F4	Q919f4 human papil
401	3	9.7	31	12	O56689	O56689 hepatitis c
402	3	9.7	31	12	Q919F2	Q919f2 human papil
403	3	9.7	31	12	Q919F1	Q919f1 human papil
404	3	9.7	31	12	O56711	O56711 hepatitis c
405	3	9.7	31	12	Q919E2	Q919e2 human papil
406	3	9.7	31	12	Q919D8	Q919d8 human papil
407	3	9.7	31	12	O56686	O56686 hepatitis c
408	3	9.7	31	12	Q9WMX5	Q9wmx5 human echov
409	3	9.7	31	12	O56690	O56690 hepatitis c
410	3	9.7	31	12	Q919E9	Q919e9 human papil
411	3	9.7	31	12	O56706	O56706 hepatitis c
412	3	9.7	31	12	O56700	O56700 hepatitis c
413	3	9.7	31	12	O56704	O56704 hepatitis c
414	3	9.7	31	12	Q919D7	Q919d7 human papil
415	3	9.7	31	12	Q919F5	Q919f5 human papil
416	3	9.7	31	12	O56693	O56693 hepatitis c
417	3	9.7	31	12	O56685	O56685 hepatitis c
418	3	9.7	31	12	O56708	O56708 hepatitis c
419	3	9.7	31	12	Q919E0	Q919e0 human papil
420	3	9.7	31	12	O56705	O56705 hepatitis c
421	3	9.7	31	12	Q919E7	Q919e7 human papil
422	3	9.7	31	12	Q914M9	Q914m9 sulfolobus
423	3	9.7	31	12	O56699	O56699 hepatitis c
424	3	9.7	31	13	O42540	O42540 brachydanio
425	3	9.7	31	13	Q91763	Q91763 xenopus lae
426	3	9.7	31	13	Q9PSU1	Q9psu1 xenopus lae
427	3	9.7	31	13	Q91816	Q91816 xenopus lae
428	3	9.7	31	15	Q83937	Q83937 ovine lenti
429	3	9.7	31	16	O25108	O25108 helicobacte
430	3	9.7	31	16	O50709	O50709 borrelia bu
431	3	9.7	31	16	O50858	O50858 borrelia bu
432	3	9.7	31	16	O51007	O51007 borrelia bu
433	3	9.7	31	16	Q9PGF2	Q9pgf2 xylella fas
434	3	9.7	31	16	Q9PAW4	Q9paw4 xylella fas
435	3	9.7	31	16	Q9KVF3	Q9kvf3 vibrio chol
436	3	9.7	31	16	Q97SZ9	Q97sz9 streptococc
437	3	9.7	31	16	Q97SW8	Q97sw8 streptococc
438	3	9.7	31	16	Q97QJ4	Q97qj4 streptococc
439	3	9.7	31	16	Q97QB7	Q97qb7 streptococc
440	3	9.7	31	16	Q97CV6	Q97cv6 streptococc
441	3	9.7	31	16	Q9K2A0	Q9k2a0 chlamydia p
442	3	9.7	31	16	Q9K236	Q9k236 chlamydia p
443	3	9.7	31	16	Q8P9W1	Q8p9w1 xanthomonas
444	3	9.7	31	16	Q8KEV8	Q8kev8 chlorobium
445	3	9.7	31	16	Q8KCQ0	Q8kcq0 chlorobium
446	3	9.7	31	16	Q8KBJ8	Q8kbj8 chlorobium
447	3	9.7	31	16	Q8EIW8	Q8eiw8 shewanella
448	3	9.7	31	16	Q8EI77	Q8ei77 shewanella
449	3	9.7	31	16	Q8E9Y5	Q8e9y5 shewanella
450	3	9.7	31	16	Q8E8G1	Q8e8g1 shewanella
451	3	9.7	31	16	Q8CTA2	Q8cta2 staphylococ
452	3	9.7	32	2	Q9AJ41	Q9aj41 buchnera ap
453	3	9.7	32	2	Q00491	Q00491 streptomyce
454	3	9.7	32	2	Q49249	Q49249 mycoplasma
455	3	9.7	32	2	Q44499	Q44499 anabaena va
456	3	9.7	32	2	Q9S629	Q9s629 prochloroco

457	3	9.7	32	2	Q8KYN3	Q8kyn3	bacillus an
458	3	9.7	32	2	Q44509	Q44509	azotobacter
459	3	9.7	32	2	Q45534	Q45534	bacillus su
460	3	9.7	32	2	Q8VN21	Q8vn21	kluuvera ci
461	3	9.7	32	2	Q9R5Q7	Q9r5q7	aeromonas h
462	3	9.7	32	2	Q8KYM4	Q8kym4	bacillus an
463	3	9.7	32	2	O32493	O32493	bacteroides
464	3	9.7	32	2	Q8VNT6	Q8vnt6	enterobacte
465	3	9.7	32	2	Q9L373	Q9l373	rhizobium l
466	3	9.7	32	2	Q8GF58	Q8gf58	zymomonas m
467	3	9.7	32	3	Q01058	Q01058	kluuveromyc
468	3	9.7	32	3	Q8TGT3	Q8tgt3	saccharomyc
469	3	9.7	32	4	Q12900	Q12900	homo sapien
470	3	9.7	32	4	Q9UEB0	Q9ueb0	homo sapien
471	3	9.7	32	4	Q8TC25	Q8tc25	homo sapien
472	3	9.7	32	4	Q96GM7	Q96gm7	homo sapien
473	3	9.7	32	4	Q9HAX8	Q9hax8	homo sapien
474	3	9.7	32	4	Q8TBQ3	Q8tbq3	homo sapien
475	3	9.7	32	4	Q96I20	Q96i20	homo sapien
476	3	9.7	32	4	Q9UN69	Q9un69	homo sapien
477	3	9.7	32	4	Q9UQV1	Q9uqv1	homo sapien
478	3	9.7	32	5	Q9GPD9	Q9gpd9	drosophila
479	3	9.7	32	5	Q8T382	Q8t382	leishmania
480	3	9.7	32	5	O96634	O96634	trypanosoma
481	3	9.7	32	5	Q9TWR8	Q9twr8	procambarus
482	3	9.7	32	5	O18606	O18606	branchiosto
483	3	9.7	32	5	Q8T757	Q8t757	branchiosto
484	3	9.7	32	6	Q9TR67	Q9tr67	sus scrofa
485	3	9.7	32	6	Q8MJ91	Q8mj91	macaca mula
486	3	9.7	32	7	Q8SNF1	Q8snf1	gallinago m
487	3	9.7	32	7	O19722	O19722	homo sapien
488	3	9.7	32	8	Q36494	Q36494	farfantepen
489	3	9.7	32	8	Q8SL89	Q8sl89	euglena ste
490	3	9.7	32	8	Q9GF95	Q9gf95	cercidiphyl
491	3	9.7	32	8	Q31736	Q31736	beta vulgar
492	3	9.7	32	8	Q8SL87	Q8sl87	euglena vir
493	3	9.7	32	8	Q31735	Q31735	beta vulgar
494	3	9.7	32	8	Q9MNM0	Q9mnm0	bufo andrew
495	3	9.7	32	8	Q9MNL0	Q9mnl0	bufo danate
496	3	9.7	32	8	Q951Q4	Q951q4	renilla ren
497	3	9.7	32	8	Q9GF72	Q9gf72	saururus ce
498	3	9.7	32	9	Q9MBU5	Q9mbu5	chlamydia p
499	3	9.7	32	10	Q8S527	Q8s527	ipomoea bat
500	3	9.7	32	10	Q8RXQ5	Q8rxq5	arabidopsis
501	3	9.7	32	10	Q40727	Q40727	oryza sativ
502	3	9.7	32	11	Q9JIU1	Q9jiu1	rattus norv
503	3	9.7	32	11	Q9R0E3	Q9r0e3	mus musculu
504	3	9.7	32	11	Q9QWM2	Q9qwm2	mus musculu
505	3	9.7	32	11	Q9QWB2	Q9qwb2	rattus sp.
506	3	9.7	32	11	Q9QXX1	Q9qxx1	mus musculu
507	3	9.7	32	11	Q8C2N8	Q8c2n8	mus musculu
508	3	9.7	32	11	Q8BS12	Q8bs12	mus musculu
509	3	9.7	32	12	Q9PXV2	Q9pxv2	hepatitis b
510	3	9.7	32	12	Q9WNI5	Q9wni5	tt virus. o
511	3	9.7	32	12	Q914F9	Q914f9	sulfolobus
512	3	9.7	32	12	Q8QYT4	Q8qyt4	grapevine v
513	3	9.7	32	12	Q8QYT7	Q8qyt7	grapevine v

514	3	9.7	32	12	Q8QYU0	Q8qyu0	grapevine v
515	3	9.7	32	12	Q9Q934	Q9q934	shope fibro
516	3	9.7	32	13	Q8QG73	Q8qg73	oncorhynchu
517	3	9.7	32	13	Q8QG72	Q8qg72	salmo salar
518	3	9.7	32	13	Q8QG71	Q8qg71	oncorhynchu
519	3	9.7	32	13	Q9PS21	Q9ps21	carassius a
520	3	9.7	32	13	Q8QG84	Q8qg84	oncorhynchu
521	3	9.7	32	13	Q8QG83	Q8qg83	oncorhynchu
522	3	9.7	32	13	Q8QG82	Q8qg82	oncorhynchu
523	3	9.7	32	13	Q8QG70	Q8qg70	salvelinus
524	3	9.7	32	13	P82780	P82780	rana catesb
525	3	9.7	32	13	Q9W7P3	Q9w7p3	morone saxa
526	3	9.7	32	13	Q9W7P2	Q9w7p2	morone saxa
527	3	9.7	32	16	O50706	O50706	borrelia bu
528	3	9.7	32	16	O50851	O50851	borrelia bu
529	3	9.7	32	16	O50865	O50865	borrelia bu
530	3	9.7	32	16	O51003	O51003	borrelia bu
531	3	9.7	32	16	Q9PGT0	Q9pgt0	xylella fas
532	3	9.7	32	16	Q9KVF7	Q9kvf7	vibrio chol
533	3	9.7	32	16	Q9KTV2	Q9ktv2	vibrio chol
534	3	9.7	32	16	Q9KPN9	Q9kpn9	vibrio chol
535	3	9.7	32	16	Q9KLF0	Q9klf0	vibrio chol
536	3	9.7	32	16	Q9K7B0	Q9k7b0	bacillus ha
537	3	9.7	32	16	Q9A2H0	Q9a2h0	caulobacter
538	3	9.7	32	16	Q98AB6	Q98ab6	rhizobium l
539	3	9.7	32	16	Q8X3V6	Q8x3v6	escherichia
540	3	9.7	32	16	Q8KG49	Q8kg49	chlorobium
541	3	9.7	32	16	Q8KEZ9	Q8kez9	chlorobium
542	3	9.7	32	16	Q8KCV3	Q8kcv3	chlorobium
543	3	9.7	32	16	Q9K4G0	Q9k4g0	streptomyce
544	3	9.7	32	16	Q8EAD5	Q8ead5	shewanella
545	3	9.7	32	16	Q8CU60	Q8cu60	staphylococ
546	3	9.7	32	16	Q8CTR7	Q8ctr7	staphylococ
547	3	9.7	32	16	Q8CRE7	Q8cre7	staphylococ
548	3	9.7	32	17	Q8ZZF7	Q8zzf7	pyrobaculum
549	3	9.7	33	1	Q9UWL4	Q9uwl4	methanopyru
550	3	9.7	33	2	Q8KH96	Q8kh96	pseudomonas
551	3	9.7	33	2	Q9S624	Q9s624	prochloroco
552	3	9.7	33	2	Q9R2M3	Q9r2m3	prochloroco
553	3	9.7	33	2	Q9X3M5	Q9x3m5	prochloroco
554	3	9.7	33	2	Q9S651	Q9s651	streptococc
555	3	9.7	33	2	Q9K533	Q9k533	listeria mo
556	3	9.7	33	2	Q9K370	Q9k370	rhizobium l
557	3	9.7	33	2	Q9S3N5	Q9s3n5	bacillus ce
558	3	9.7	33	2	Q8KQ80	Q8kq80	vibrio chol
559	3	9.7	33	2	Q56414	Q56414	escherichia
560	3	9.7	33	2	Q9S622	Q9s622	prochloroco
561	3	9.7	33	2	Q9K2V1	Q9k2v1	rhizobium l
562	3	9.7	33	2	Q9F1F4	Q9f1f4	enterococcu
563	3	9.7	33	2	Q9KI23	Q9ki23	helicobacte
564	3	9.7	33	2	Q8GQU2	Q8gqu2	leptospira
565	3	9.7	33	3	Q8TGR1	Q8tgr1	saccharomyc
566	3	9.7	33	4	Q99950	Q99950	homo sapien
567	3	9.7	33	4	Q9UP36	Q9up36	homo sapien
568	3	9.7	33	4	Q15285	Q15285	homo sapien
569	3	9.7	33	4	Q9UDI1	Q9udi1	homo sapien
570	3	9.7	33	4	Q9P1T8	Q9plt8	homo sapien

571	3	9.7	33	4	Q9BV16	Q9bv16	homo sapien
572	3	9.7	33	4	Q92668	Q92668	homo sapien
573	3	9.7	33	5	Q9GTB2	Q9gtb2	eimeria ten
574	3	9.7	33	5	Q9GT93	Q9gt93	cryptospori
575	3	9.7	33	5	Q26673	Q26673	tethya aura
576	3	9.7	33	5	Q26672	Q26672	tethya aura
577	3	9.7	33	5	Q9GTC2	Q9gtc2	plasmodium
578	3	9.7	33	5	Q27637	Q27637	drosophila
579	3	9.7	33	5	Q9GTB3	Q9gtb3	eimeria ten
580	3	9.7	33	5	Q9GTA6	Q9gta6	sarcocystis
581	3	9.7	33	5	Q9GTA1	Q9gta1	babesia bov
582	3	9.7	33	5	Q17293	Q17293	cancer ante
583	3	9.7	33	5	Q27310	Q27310	paramecium
584	3	9.7	33	5	Q9GTA9	Q9gta9	sarcocystis
585	3	9.7	33	5	O17147	O17147	echinococcu
586	3	9.7	33	5	Q9GT95	Q9gt95	cryptospori
587	3	9.7	33	5	Q9GTA2	Q9gta2	babesia bov
588	3	9.7	33	6	Q28788	Q28788	papio hamad
589	3	9.7	33	6	O18916	O18916	sus scrofa
590	3	9.7	33	6	Q9TSX7	Q9tsx7	sus scrofa
591	3	9.7	33	6	Q95M05	Q95m05	bos taurus
592	3	9.7	33	7	Q8MGU2	Q8mgu2	bos taurus
593	3	9.7	33	7	Q8SNF0	Q8snf0	gallinago m
594	3	9.7	33	8	Q9BAC6	Q9bac6	euglena gra
595	3	9.7	33	8	Q8W9G0	Q8w9g0	meloidogyne
596	3	9.7	33	8	Q9BAC1	Q9bac1	euglena ste
597	3	9.7	33	8	Q9XNP3	Q9xnp3	boophilus m
598	3	9.7	33	8	O78857	O78857	phytophthor
599	3	9.7	33	8	Q9T2N1	Q9t2n1	nicotiana t
600	3	9.7	33	8	Q9BAC4	Q9bac4	euglena mut
601	3	9.7	33	8	Q8WEJ5	Q8wej5	ginkgo bilo
602	3	9.7	33	8	Q8HUH3	Q8huh3	chlamydomon
603	3	9.7	33	8	Q8HS33	Q8hs33	hydrastis c
604	3	9.7	33	9	Q38588	Q38588	bacteriopha
605	3	9.7	33	9	Q38551	Q38551	bacteriopha
606	3	9.7	33	10	O49775	O49775	arabidopsis
607	3	9.7	33	10	Q9S8V5	Q9s8v5	zea mays (m
608	3	9.7	33	10	Q9AYQ5	Q9ayq5	cucumis sat
609	3	9.7	33	11	Q9QVM2	Q9qvm2	mus sp. glu
610	3	9.7	33	12	O72982	O72982	hepatitis c
611	3	9.7	33	12	O73068	O73068	hepatitis c
612	3	9.7	33	12	Q90085	Q90085	human papil
613	3	9.7	33	12	O72979	O72979	hepatitis c
614	3	9.7	33	12	Q91J04	Q91j04	tt virus. o
615	3	9.7	33	12	O72996	O72996	hepatitis c
616	3	9.7	33	12	Q91J14	Q91j14	tt virus. o
617	3	9.7	33	12	O72988	O72988	hepatitis c
618	3	9.7	33	12	O72992	O72992	hepatitis c
619	3	9.7	33	12	Q91J12	Q91j12	tt virus. o
620	3	9.7	33	12	Q91J15	Q91j15	tt virus. o
621	3	9.7	33	12	Q91J07	Q91j07	tt virus. o
622	3	9.7	33	12	O72995	O72995	hepatitis c
623	3	9.7	33	12	Q91J09	Q91j09	tt virus. o
624	3	9.7	33	12	O72990	O72990	hepatitis c
625	3	9.7	33	12	O73010	O73010	hepatitis c
626	3	9.7	33	12	Q86912	Q86912	hepatitis c
627	3	9.7	33	12	Q8V5G7	Q8v5g7	hepatitis c

628	3	9.7	33	12	072981	072981 hepatitis c
629	3	9.7	33	12	Q91J08	Q91j08 tt virus. o
630	3	9.7	33	12	072997	072997 hepatitis c
631	3	9.7	33	12	073008	073008 hepatitis c
632	3	9.7	33	12	Q83963	Q83963 avian influ
633	3	9.7	33	12	072986	072986 hepatitis c
634	3	9.7	33	12	072993	072993 hepatitis c
635	3	9.7	33	12	Q91J06	Q91j06 tt virus. o
636	3	9.7	33	12	072984	072984 hepatitis c
637	3	9.7	33	12	073005	073005 hepatitis c
638	3	9.7	33	12	073067	073067 hepatitis c
639	3	9.7	33	12	072985	072985 hepatitis c
640	3	9.7	33	12	072999	072999 hepatitis c
641	3	9.7	33	12	Q91J16	Q91j16 tt virus. o
642	3	9.7	33	12	072998	072998 hepatitis c
643	3	9.7	33	12	Q91J11	Q91j11 tt virus. o
644	3	9.7	33	12	072994	072994 hepatitis c
645	3	9.7	33	12	Q8V5H0	Q8v5h0 hepatitis c
646	3	9.7	33	12	Q91J13	Q91j13 tt virus. o
647	3	9.7	33	12	Q8V5G8	Q8v5g8 hepatitis c
648	3	9.7	33	12	072983	072983 hepatitis c
649	3	9.7	33	12	073007	073007 hepatitis c
650	3	9.7	33	12	Q91J10	Q91j10 tt virus. o
651	3	9.7	33	12	072987	072987 hepatitis c
652	3	9.7	33	12	Q91J17	Q91j17 tt virus. o
653	3	9.7	33	12	Q69461	Q69461 human herpe
654	3	9.7	33	12	Q8V5G9	Q8v5g9 hepatitis c
655	3	9.7	33	12	072978	072978 hepatitis c
656	3	9.7	33	12	073009	073009 hepatitis c
657	3	9.7	33	12	073004	073004 hepatitis c
658	3	9.7	33	12	Q99138	Q99138 avian influ
659	3	9.7	33	13	P82740	P82740 rana tempor
660	3	9.7	33	13	P82236	P82236 rana tempor
661	3	9.7	33	15	Q9DZ98	Q9dz98 human immun
662	3	9.7	33	15	Q86107	Q86107 simian sarc
663	3	9.7	33	16	Q9PA23	Q9pa23 xylella fas
664	3	9.7	33	16	Q9KQP4	Q9kqp4 vibrio chol
665	3	9.7	33	16	Q9KML1	Q9kml1 vibrio chol
666	3	9.7	33	16	Q97T91	Q97t91 streptococc
667	3	9.7	33	16	Q97PC1	Q97pc1 streptococc
668	3	9.7	33	16	Q932N2	Q932n2 staphylococ
669	3	9.7	33	16	Q8ZKL2	Q8zkl2 salmonella
670	3	9.7	33	16	Q8Z1V4	Q8z1v4 salmonella
671	3	9.7	33	16	Q8U5M4	Q8u5m4 agrobacteri
672	3	9.7	33	16	Q8VK01	Q8vk01 mycobacteri
673	3	9.7	33	16	Q8NUL1	Q8nul1 staphylococ
674	3	9.7	33	16	Q8NT95	Q8nt95 corynebacte
675	3	9.7	33	16	Q8NLP2	Q8nlp2 corynebacte
676	3	9.7	33	16	Q8KG99	Q8kg99 chlorobium
677	3	9.7	33	16	Q8KBZ0	Q8kbz0 chlorobium
678	3	9.7	33	16	Q8G0U8	Q8g0u8 brucella su
679	3	9.7	33	16	Q8FZ67	Q8fz67 brucella su
680	3	9.7	33	16	Q8FYR6	Q8fyr6 brucella su
681	3	9.7	33	16	Q8FY86	Q8fy86 brucella su
682	3	9.7	33	16	Q8FSG0	Q8fsg0 corynebacte
683	3	9.7	33	16	Q8EJH6	Q8ejh6 shewanella
684	3	9.7	33	16	Q8EGA9	Q8ega9 shewanella

685	3	9.7	33	16	Q8EE59	Q8ee59 shewanella
686	3	9.7	33	16	Q8EE42	Q8ee42 shewanella
687	3	9.7	33	16	Q8E8W4	Q8e8w4 shewanella
688	3	9.7	33	16	Q8E1Y5	Q8ely5 streptococc
689	3	9.7	33	16	Q8CTR8	Q8ctr8 staphylococ
690	3	9.7	33	16	Q8CQY7	Q8cqy7 staphylococ
691	3	9.7	33	17	Q9HSX6	Q9hsx6 halobacteri
692	3	9.7	33	17	Q8U2X8	Q8u2x8 pyrococcus
693	3	9.7	34	2	Q54427	Q54427 spiroplasma
694	3	9.7	34	2	Q9X3L6	Q9x3l6 prochloroco
695	3	9.7	34	2	Q9R5U1	Q9r5u1 campylobact
696	3	9.7	34	2	Q44208	Q44208 pseudomonas
697	3	9.7	34	2	Q9X7J6	Q9x7j6 pseudomonas
698	3	9.7	34	2	Q8KYH2	Q8kyh2 bacillus an
699	3	9.7	34	2	O31061	O31061 butyrivibri
700	3	9.7	34	2	Q9R8A2	Q9r8a2 chlamydia t
701	3	9.7	34	2	Q9RZW6	Q9rzw6 borrelia bu
702	3	9.7	34	2	Q8GJC8	Q8gjc8 campylobact
703	3	9.7	34	2	Q8G8C9	Q8g8c9 pseudomonas
704	3	9.7	34	3	Q00377	Q00377 coccidioide
705	3	9.7	34	4	Q99910	Q99910 homo sapien
706	3	9.7	34	4	Q9H3R8	Q9h3r8 homo sapien
707	3	9.7	34	4	Q9UI64	Q9ui64 homo sapien
708	3	9.7	34	4	Q8WY57	Q8wy57 homo sapien
709	3	9.7	34	4	Q8WW51	Q8ww51 homo sapien
710	3	9.7	34	4	Q9BSP7	Q9bsp7 homo sapien
711	3	9.7	34	4	Q9H4L8	Q9h4l8 homo sapien
712	3	9.7	34	4	Q8NEQ3	Q8neq3 homo sapien
713	3	9.7	34	4	Q15251	Q15251 homo sapien
714	3	9.7	34	4	Q9NQY9	Q9nqy9 homo sapien
715	3	9.7	34	5	Q9BIP7	Q9bip7 cooperia pu
716	3	9.7	34	5	Q27821	Q27821 trichomonas
717	3	9.7	34	5	Q9GQE5	Q9gqe5 branchiosto
718	3	9.7	34	6	Q9TS91	Q9ts91 oryctolagus
719	3	9.7	34	6	P79429	P79429 capra hircu
720	3	9.7	34	6	Q9TRI2	Q9tri2 sus scrofa
721	3	9.7	34	6	P82908	P82908 bos taurus
722	3	9.7	34	8	O79025	O79025 enallagma v
723	3	9.7	34	8	Q9T2T7	Q9t2t7 bos taurus
724	3	9.7	34	8	Q8MCA2	Q8mca2 phaseolus a
725	3	9.7	34	8	Q8HKE1	Q8hke1 rhipicephal
726	3	9.7	34	10	Q8W2H0	Q8w2h0 paspalum no
727	3	9.7	34	10	Q8VWL0	Q8vwl0 paspalum no
728	3	9.7	34	10	Q9SCA3	Q9sca3 lycopersico
729	3	9.7	34	11	Q923Z1	Q923z1 mus musculu
730	3	9.7	34	11	Q8R557	Q8r557 mus musculu
731	3	9.7	34	11	Q9ET72	Q9et72 mus musculu
732	3	9.7	34	11	Q99KM9	Q99km9 mus musculu
733	3	9.7	34	11	Q99KX7	Q99kx7 mus musculu
734	3	9.7	34	11	Q64170	Q64170 mus sp. b-r
735	3	9.7	34	11	Q8VHL4	Q8vhl4 rattus norv
736	3	9.7	34	12	Q9DW68	Q9dw68 rat cytomeg
737	3	9.7	34	13	O42521	O42521 scyliorhinu
738	3	9.7	34	13	O13101	O13101 ambystoma m
739	3	9.7	34	13	Q8QGG2	Q8qgg2 oncorhynchu
740	3	9.7	34	13	Q8QFM9	Q8qfm9 oncorhynchu
741	3	9.7	34	13	O42526	O42526 scyliorhinu

742	3	9.7	34	13	Q9PRE7	Q9pre7 oryzias lat
743	3	9.7	34	13	Q8QGG1	Q8qgg1 oncorhynch
744	3	9.7	34	13	Q8QGF7	Q8qgf7 oncorhynch
745	3	9.7	34	13	Q98TM8	Q98tm8 platichthys
746	3	9.7	34	15	O40445	O40445 human immun
747	3	9.7	34	15	Q9WR32	Q9wr32 human immun
748	3	9.7	34	15	Q9W8Y1	Q9w8y1 chimpanzee
749	3	9.7	34	16	O50812	O50812 borrelia bu
750	3	9.7	34	16	O50877	O50877 borrelia bu
751	3	9.7	34	16	Q9PGH3	Q9pgh3 xylella fas
752	3	9.7	34	16	Q9PGF8	Q9pgf8 xylella fas
753	3	9.7	34	16	Q9PFA5	Q9pfa5 xylella fas
754	3	9.7	34	16	Q9PDD0	Q9pdd0 xylella fas
755	3	9.7	34	16	Q9KRA8	Q9kra8 vibrio chol
756	3	9.7	34	16	Q9KPW9	Q9kpw9 vibrio chol
757	3	9.7	34	16	Q9KM63	Q9km63 vibrio chol
758	3	9.7	34	16	Q9K7C6	Q9k7c6 bacillus ha
759	3	9.7	34	16	Q9JY24	Q9jy24 neisseria m
760	3	9.7	34	16	Q9JVP3	Q9jvp3 neisseria m
761	3	9.7	34	16	Q9JUR9	Q9jur9 neisseria m
762	3	9.7	34	16	Q97SF7	Q97sf7 streptococc
763	3	9.7	34	16	Q97PI6	Q97pi6 streptococc
764	3	9.7	34	16	Q9K2B9	Q9k2b9 chlamydia p
765	3	9.7	34	16	Q8X4V1	Q8x4v1 escherichia
766	3	9.7	34	16	Q8U5V2	Q8u5v2 agrobacteri
767	3	9.7	34	16	Q8VIY1	Q8viy1 mycobacteri
768	3	9.7	34	16	Q8RIC7	Q8ric7 fusobacteri
769	3	9.7	34	16	Q8NWX3	Q8nwx3 staphylococ
770	3	9.7	34	16	Q8NV10	Q8nv10 staphylococ
771	3	9.7	34	16	Q8KEQ8	Q8keq8 chlorobium
772	3	9.7	34	16	Q8KEL5	Q8kel5 chlorobium
773	3	9.7	34	16	Q8KDE4	Q8kde4 chlorobium
774	3	9.7	34	16	Q8F830	Q8f830 leptospira
775	3	9.7	34	16	Q8F827	Q8f827 leptospira
776	3	9.7	34	16	Q8F5Y7	Q8f5y7 leptospira
777	3	9.7	34	16	Q8F0V9	Q8f0v9 leptospira
778	3	9.7	34	16	Q8EZR6	Q8ezr6 leptospira
779	3	9.7	34	16	Q8EZ37	Q8ez37 leptospira
780	3	9.7	34	16	Q8EYG6	Q8eyg6 leptospira
781	3	9.7	34	16	Q8EXH6	Q8exh6 leptospira
782	3	9.7	34	16	Q8EXA8	Q8exa8 leptospira
783	3	9.7	34	16	Q8EJ65	Q8ej65 shewanella
784	3	9.7	34	16	Q8EI45	Q8ei45 shewanella
785	3	9.7	34	16	Q8EHU5	Q8ehu5 shewanella
786	3	9.7	34	16	Q8E8Y3	Q8e8y3 shewanella
787	3	9.7	34	16	Q8E8W3	Q8e8w3 shewanella
788	3	9.7	34	16	Q8E173	Q8e173 streptococc
789	3	9.7	34	16	Q8CRY3	Q8cry3 staphylococ
790	3	9.7	34	17	Q8U1I1	Q8ul11 pyrococcus
791	3	9.7	35	2	Q9R624	Q9r624 bacillus su
792	3	9.7	35	2	Q9JPG9	Q9jpg9 neisseria m
793	3	9.7	35	2	Q9R625	Q9r625 bacillus su
794	3	9.7	35	2	Q9X3D6	Q9x3d6 prochloroco
795	3	9.7	35	2	Q9R5I3	Q9r5i3 thermoanaer
796	3	9.7	35	2	Q9FCX4	Q9fcx4 clostridium
797	3	9.7	35	2	Q9XBK0	Q9xbk0 bacillus ce
798	3	9.7	35	2	Q53564	Q53564 neisseria g

799	3	9.7	35	2	Q46537	Q46537 bacteroides
800	3	9.7	35	2	Q9ZG35	Q9zg35 chlamydia t
801	3	9.7	35	2	Q9RHG5	Q9rhg5 bacillus ce
802	3	9.7	35	2	Q9R4A1	Q9r4a1 klebsiella
803	3	9.7	35	2	O30661	O30661 vibrio chol
804	3	9.7	35	2	Q9ZG68	Q9zg68 chlamydia t
805	3	9.7	35	2	Q8RKG3	Q8rkg3 clostridium
806	3	9.7	35	2	Q8RIW2	Q8riw2 clostridium
807	3	9.7	35	2	Q9R626	Q9r626 bacillus su
808	3	9.7	35	2	P81927	P81927 lactobacill
809	3	9.7	35	3	Q96UT3	Q96ut3 saccharomyc
810	3	9.7	35	4	Q9BVR9	Q9bvr9 homo sapien
811	3	9.7	35	4	Q13380	Q13380 homo sapien
812	3	9.7	35	4	Q9BS62	Q9bs62 homo sapien
813	3	9.7	35	4	Q13165	Q13165 homo sapien
814	3	9.7	35	4	Q13828	Q13828 homo sapien
815	3	9.7	35	4	Q13264	Q13264 homo sapien
816	3	9.7	35	4	Q9Y634	Q9y634 homo sapien
817	3	9.7	35	4	Q9BU09	Q9bu09 homo sapien
818	3	9.7	35	4	Q8IU77	Q8iu77 homo sapien
819	3	9.7	35	5	Q27754	Q27754 pisaster oc
820	3	9.7	35	5	Q9U780	Q9u780 boophilus a
821	3	9.7	35	5	Q26372	Q26372 tribolium c
822	3	9.7	35	5	Q9U782	Q9u782 boophilus m
823	3	9.7	35	5	Q9TVJ7	Q9tvj7 boophilus m
824	3	9.7	35	5	Q9U783	Q9u783 boophilus m
825	3	9.7	35	5	Q9U784	Q9u784 boophilus m
826	3	9.7	35	5	Q9U781	Q9u781 boophilus m
827	3	9.7	35	5	Q8IF21	Q8if21 trypanosoma
828	3	9.7	35	6	Q95N74	Q95n74 equus cabal
829	3	9.7	35	6	Q9MZA7	Q9mza7 sus scrofa
830	3	9.7	35	8	Q951Q6	Q951q6 protoptilum
831	3	9.7	35	8	Q8W7S9	Q8w7s9 colpomenia
832	3	9.7	35	8	Q9GF85	Q9gf85 ginkgo bilo
833	3	9.7	35	8	Q8W7T0	Q8w7t0 petalonia b
834	3	9.7	35	8	Q8W7S8	Q8w7s8 petalonia f
835	3	9.7	35	8	Q8WE70	Q8we70 miliaria ca
836	3	9.7	35	8	Q8W7S7	Q8w7s7 scytosiphon
837	3	9.7	35	8	Q9GF98	Q9gf98 ceratophyll
838	3	9.7	35	8	Q95766	Q95766 cerataphis
839	3	9.7	35	8	Q94P82	Q94p82 corallium r
840	3	9.7	35	8	Q8WEJ7	Q8wej7 cycas circi
841	3	9.7	35	8	Q951S7	Q951s7 anthothela
842	3	9.7	35	8	Q951R1	Q951r1 narella nut
843	3	9.7	35	8	Q951S1	Q951s1 corallium k
844	3	9.7	35	8	Q8WII3	Q8wii3 colpomenia
845	3	9.7	35	8	Q951R3	Q951r3 anthomurice
846	3	9.7	35	8	Q8WIH9	Q8wih9 scytosiphon
847	3	9.7	35	8	Q8WIH5	Q8wih5 hydroclathr
848	3	9.7	35	8	Q951S9	Q951s9 protodendro
849	3	9.7	35	8	Q8WII1	Q8wii1 scytosiphon
850	3	9.7	35	8	Q951Q9	Q951q9 narella sp.
851	3	9.7	35	8	Q951S4	Q951s4 paragorgia
852	3	9.7	35	8	Q951R5	Q951r5 corallium s
853	3	9.7	35	10	Q9SPU2	Q9spu2 arabidopsis
854	3	9.7	35	10	Q9MAB1	Q9mab1 arabidopsis
855	3	9.7	35	10	Q9ZUW2	Q9zuw2 arabidopsis

856	3	9.7	35	10	P92971	P92971	arabidopsis
857	3	9.7	35	10	Q9LV08	Q9lv08	arabidopsis
858	3	9.7	35	10	Q9LQ64	Q9lq64	arabidopsis
859	3	9.7	35	10	Q94IS4	Q94is4	pinus radia
860	3	9.7	35	10	Q39297	Q39297	brassica na
861	3	9.7	35	10	Q8RVJ7	Q8rvj7	populus eur
862	3	9.7	35	10	Q9FJ84	Q9fj84	arabidopsis
863	3	9.7	35	10	Q8GUX4	Q8gux4	picea maria
864	3	9.7	35	11	Q63397	Q63397	rattus norv
865	3	9.7	35	11	Q9JIA4	Q9jla4	mus musculu
866	3	9.7	35	11	Q60608	Q60608	mus musculu
867	3	9.7	35	11	Q9QV50	Q9qv50	rattus sp.
868	3	9.7	35	11	Q9QV30	Q9qv30	rattus sp.
869	3	9.7	35	11	Q922H5	Q922h5	mus musculu
870	3	9.7	35	11	Q8BK89	Q8bk89	mus musculu
871	3	9.7	35	12	Q90151	Q90151	bombyx mori
872	3	9.7	35	12	Q65380	Q65380	banana bunc
873	3	9.7	35	12	Q83333	Q83333	murine hepa
874	3	9.7	35	12	O55549	O55549	measles vir
875	3	9.7	35	12	Q8BB50	Q8bb50	human papil
876	3	9.7	35	13	Q90XB5	Q90xb5	xenopus lae
877	3	9.7	35	13	P83224	P83224	oxyuranus m
878	3	9.7	35	13	P83225	P83225	oxyuranus s
879	3	9.7	35	13	P83227	P83227	oxyuranus m
880	3	9.7	35	13	P83228	P83228	oxyuranus s
881	3	9.7	35	13	P83229	P83229	oxyuranus s
882	3	9.7	35	13	P83226	P83226	oxyuranus s
883	3	9.7	35	15	Q75981	Q75981	human immun
884	3	9.7	35	15	Q70328	Q70328	human immun
885	3	9.7	35	15	Q70380	Q70380	human immun
886	3	9.7	35	15	Q70319	Q70319	human immun
887	3	9.7	35	15	Q79465	Q79465	human immun
888	3	9.7	35	15	Q70426	Q70426	human immun
889	3	9.7	35	15	Q9J3S2	Q9j3s2	human immun
890	3	9.7	35	15	O71950	O71950	human immun
891	3	9.7	35	15	Q9IPY2	Q9ipy2	human immun
892	3	9.7	35	15	Q80574	Q80574	human immun
893	3	9.7	35	15	Q70425	Q70425	human immun
894	3	9.7	35	15	Q70362	Q70362	human immun
895	3	9.7	35	15	Q80601	Q80601	human immun
896	3	9.7	35	15	Q8QDX6	Q8qdx6	human immun
897	3	9.7	35	15	Q77702	Q77702	human immun
898	3	9.7	35	15	Q9QFA0	Q9qfa0	human immun
899	3	9.7	35	15	Q70330	Q70330	human immun
900	3	9.7	35	15	Q77584	Q77584	human immun
901	3	9.7	35	15	Q70317	Q70317	human immun
902	3	9.7	35	15	Q70316	Q70316	human immun
903	3	9.7	35	15	Q70402	Q70402	human immun
904	3	9.7	35	15	Q9YM80	Q9ym80	human immun
905	3	9.7	35	15	Q8QDY0	Q8qdy0	human immun
906	3	9.7	35	15	Q75970	Q75970	human immun
907	3	9.7	35	15	Q70409	Q70409	human immun
908	3	9.7	35	15	Q70325	Q70325	human immun
909	3	9.7	35	15	Q9YM17	Q9ym17	human immun
910	3	9.7	35	15	Q79468	Q79468	human immun
911	3	9.7	35	15	Q9YM96	Q9ym96	human immun
912	3	9.7	35	15	Q70363	Q70363	human immun

913	3	9.7	35	15	Q70321	Q70321 human immun
914	3	9.7	35	15	Q9YM22	Q9ym22 human immun
915	3	9.7	35	15	Q75990	Q75990 human immun
916	3	9.7	35	15	Q70323	Q70323 human immun
917	3	9.7	35	15	Q75989	Q75989 human immun
918	3	9.7	35	15	Q70428	Q70428 human immun
919	3	9.7	35	15	Q9YM67	Q9ym67 human immun
920	3	9.7	35	15	Q77585	Q77585 human immun
921	3	9.7	35	15	Q70403	Q70403 human immun
922	3	9.7	35	15	Q70327	Q70327 human immun
923	3	9.7	35	15	Q77250	Q77250 human immun
924	3	9.7	35	15	Q75955	Q75955 human immun
925	3	9.7	35	15	Q9IPY4	Q9ipy4 human immun
926	3	9.7	35	15	Q70424	Q70424 human immun
927	3	9.7	35	15	Q77582	Q77582 human immun
928	3	9.7	35	16	O07593	O07593 bacillus su
929	3	9.7	35	16	Q9KR18	Q9kr18 vibrio chol
930	3	9.7	35	16	Q9KNU1	Q9knu1 vibrio chol
931	3	9.7	35	16	Q9JWX5	Q9jwx5 neisseria m
932	3	9.7	35	16	Q9JV38	Q9jv38 neisseria m
933	3	9.7	35	16	Q9A427	Q9a427 caulobacter
934	3	9.7	35	16	Q9K241	Q9k241 chlamydia p
935	3	9.7	35	16	Q8XZB7	Q8xzb7 ralstonia s
936	3	9.7	35	16	Q8X4F4	Q8x4f4 escherichia
937	3	9.7	35	16	Q8KCA6	Q8kca6 chlorobium
938	3	9.7	35	16	Q8G2D4	Q8g2d4 brucella su
939	3	9.7	35	16	Q8F9H5	Q8f9h5 leptospira
940	3	9.7	35	16	Q8F8D4	Q8f8d4 leptospira
941	3	9.7	35	16	Q8F1W8	Q8f1w8 leptospira
942	3	9.7	35	16	Q8EYH6	Q8eyh6 leptospira
943	3	9.7	35	16	Q8EGT2	Q8egt2 shewanella
944	3	9.7	35	16	Q8EGC0	Q8egc0 shewanella
945	3	9.7	35	16	Q8EG97	Q8eg97 shewanella
946	3	9.7	35	16	Q8EEP3	Q8eep3 shewanella
947	3	9.7	35	16	Q8E9Z1	Q8e9z1 shewanella
948	3	9.7	35	16	Q8DUY1	Q8duy1 streptococc
949	3	9.7	35	17	Q9HMP1	Q9hmp1 halobacteri
950	3	9.7	35	17	Q8ZXX9	Q8zxx9 pyrobaculum
951	3	9.7	36	2	O06954	O06954 salmonella
952	3	9.7	36	2	Q8VTS7	Q8vts7 listeria in
953	3	9.7	36	2	Q9ZG79	Q9zg79 chlamydia t
954	3	9.7	36	2	Q9RHE3	Q9rhe3 pediococcus
955	3	9.7	36	2	Q8VTS5	Q8vts5 listeria we
956	3	9.7	36	2	Q44437	Q44437 agrobacteri
957	3	9.7	36	2	Q91B55	Q91b55 helicobacte
958	3	9.7	36	2	Q48507	Q48507 lactococcus
959	3	9.7	36	2	Q99094	Q99094 salmonella
960	3	9.7	36	2	Q9S635	Q9s635 prochloroco
961	3	9.7	36	2	Q8VTR8	Q8vtr8 listeria iv
962	3	9.7	36	2	Q8VTS0	Q8vts0 listeria mo
963	3	9.7	36	2	Q8KYW1	Q8kyw1 uncultured
964	3	9.7	36	2	Q9R4X9	Q9r4x9 azotobacter
965	3	9.7	36	2	Q9R5L0	Q9r5l0 sarcina ven
966	3	9.7	36	2	Q9X3G2	Q9x3g2 prochloroco
967	3	9.7	36	2	Q9R536	Q9r536 sphingomona
968	3	9.7	36	2	Q8GRH1	Q8grh1 pectobacter
969	3	9.7	36	3	Q96W36	Q96w36 ophiostoma

970	3	9.7	36	4	Q9UNV7	Q9unv7 homo sapien
971	3	9.7	36	4	Q9P1E9	Q9ple9 homo sapien
972	3	9.7	36	4	Q9UPB7	Q9upb7 homo sapien
973	3	9.7	36	4	Q8NE47	Q8ne47 homo sapien
974	3	9.7	36	5	Q9GSY9	Q9gsy9 carcinus ma
975	3	9.7	36	5	Q9NGN1	Q9ngn1 strongyloce
976	3	9.7	36	5	Q27730	Q27730 plasmodium
977	3	9.7	36	5	Q9GNP3	Q9gnp3 caenorhabdi
978	3	9.7	36	5	O01333	O01333 caenorhabdi
979	3	9.7	36	5	Q25781	Q25781 plasmodium
980	3	9.7	36	5	Q8ISR7	Q8isr7 spodoptera
981	3	9.7	36	5	Q8IGF5	Q8igf5 drosophila
982	3	9.7	36	6	O97889	O97889 pongo pygma
983	3	9.7	36	6	Q29059	Q29059 sus scrofa
984	3	9.7	36	6	Q9XT44	Q9xt44 pongo pygma
985	3	9.7	36	6	Q9N1C5	Q9n1c5 bos taurus
986	3	9.7	36	6	O97890	O97890 pan troglod
987	3	9.7	36	6	P79428	P79428 capra hircu
988	3	9.7	36	8	O63675	O63675 emberiza pu
989	3	9.7	36	8	Q9GF81	Q9gf81 gnetum gnem
990	3	9.7	36	8	Q9TIE4	Q9tie4 hydrocotyle
991	3	9.7	36	8	Q9TIF1	Q9tif1 bolax gummi
992	3	9.7	36	8	Q9GFA3	Q9gfa3 cabomba car
993	3	9.7	36	8	Q9GF97	Q9gf97 ceratophyll
994	3	9.7	36	8	Q94VL4	Q94vl4 salmo trutt
995	3	9.7	36	8	Q36303	Q36303 musa schizo
996	3	9.7	36	8	Q9TIF0	Q9tif0 klotzschia
997	3	9.7	36	8	Q94NY5	Q94ny5 salmo salar
998	3	9.7	36	8	Q9GF76	Q9gf76 lactoris fe
999	3	9.7	36	8	Q9MSP9	Q9msp9 nymphaea od
1000	3	9.7	36	8	Q9TIF3	Q9tif3 eremocharis

ALIGNMENTS

RESULT 1

Q91Y90

ID Q91Y90 PRELIMINARY; PRT; 31 AA.

AC Q91Y90;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)

DE Parathyroid hormone (Fragment).

GN PTH.

OS Peromyscus maniculatus (Deer mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;

OC Peromyscus.

OX NCBI_TaxID=10042;

RN [1]

RP SEQUENCE FROM N.A.

RA Prince K.L., Dewey M.J.;

RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.

DR EMBL; AF382953; AAK63072.1; -.

DR InterPro; IPR001415; Parathyrd_hrm.

DR InterPro; IPR003625; Pthyrhorm_sub.

DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 45.2%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHL 15
|||
Db 14 VSEIQLMHNLGKHL 27

RESULT 2

Q91Y91

ID Q91Y91 PRELIMINARY; PRT; 31 AA.
AC Q91Y91;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Parathyroid hormone (Fragment).
GN PTH.
OS Peromyscus polionotus (Oldfield mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Sigmodontinae;
OC Peromyscus.
OX NCBI_TaxID=42413;
RN [1]
RP SEQUENCE FROM N.A.
RA Prince K.L., Dewey M.J.;
RL Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF382952; AAK63071.1; -.
DR InterPro; IPR001415; Parathyrd_hrm.
DR InterPro; IPR003625; Pthyrhorm_sub.
DR Pfam; PF01279; Parathyroid; 1.
DR ProDom; PD010687; Pthyrhorm_sub; 1.
DR PROSITE; PS00335; PARATHYROID; 1.
FT NON_TER 1 1
FT NON_TER 31 31
SQ SEQUENCE 31 AA; 3461 MW; A208B0E772B9B55B CRC64;

Query Match 45.2%; Score 14; DB 11; Length 31;
Best Local Similarity 100.0%; Pred. No. 4.9e-08;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VSEIQLMHNLGKHL 15
|||
Db 14 VSEIQLMHNLGKHL 27

RESULT 3

O17148

ID O17148 PRELIMINARY; PRT; 34 AA.
AC O17148;

DT 01-JAN-1998 (TrEMBLrel. 05, Created)
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Antigen B/1 (Fragment).
 GN AGB/1.
 OS Echinococcus vogeli.
 OC Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
 OC Cyclophyllidea; Taeniidae; Echinococcus.
 OX NCBI_TaxID=6213;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94359533; PubMed=8078520;
 RA Frosch P., Hartmann M., Muhlschlegel F., Frosch M.;
 RT "Sequence heterogeneity of the echinococcal antigen B.";
 RL Mol. Biochem. Parasitol. 64:171-175(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Haag K.L., Zaha A., Gottstein B.;
 RT "E. vogeli AgB/1 coding sequence.";
 RL Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF024665; AAB81611.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 3964 MW; 3BE894E129CF84F3 CRC64;

Query Match 16.1%; Score 5; DB 5; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKKL 28
 |||||
 Db 15 LRKKL 19

RESULT 4

Q97K50

ID Q97K50 PRELIMINARY; PRT; 34 AA.
 AC Q97K50;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
 DE Transcriptional regulator, AcrR family.
 GN CAC1071.
 OS Clostridium acetobutylicum.
 OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
 OC Clostridium.
 OX NCBI_TaxID=1488;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
 RX MEDLINE=21359325; PubMed=11466286;
 RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
 RA Gibson R., Lee H.M., Dubois J., Qiu D., Hitti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.;
 RT "Genome sequence and comparative analysis of the solvent-producing
 bacterium Clostridium acetobutylicum.";

RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL; AE007622; AAK79045.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 4031 MW; 38D1A2A7C2F86E90 CRC64;

Query Match 16.1%; Score 5; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5
|||||
Db 30 SVSEI 34

RESULT 5

Q9HR65

ID Q9HR65 PRELIMINARY; PRT; 34 AA.
AC Q9HR65;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DE Vng0840h.
GN VNG0840H.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
OC Halobacteriaceae; Halobacterium.
OX NCBI_TaxID=64091;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20504483; PubMed=11016950;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
RT "Genome sequence of Halobacterium species NRC-1."
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
DR EMBL; AE005025; AAG19293.1; -.
KW Complete proteome.
SQ SEQUENCE 34 AA; 3731 MW; BA957904338DCD45 CRC64;

Query Match 16.1%; Score 5; DB 17; Length 34;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKKL 28
|||||
Db 26 LRKKL 30

RESULT 6

Q8BTB9

ID Q8BTB9 PRELIMINARY; PRT; 35 AA.
AC Q8BTB9;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Translin.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Body;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs.";
 RL Nature 420:563-573(2002).
 DR EMBL; AK011220; BAC25325.1; -.
 SQ SEQUENCE 35 AA; 3967 MW; F81156686390ECD8 CRC64;

Query Match 16.1%; Score 5; DB 11; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SVSEI 5
 |||||
 Db 2 SVSEI 6

RESULT 7

Q97RG6

ID Q97RG6 PRELIMINARY; PRT; 35 AA.
 AC Q97RG6;
 DT 01-OCT-2001 (TrEMBLrel. 18, Created)
 DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Hypothetical protein SP0853.
 GN SP0853.
 OS Streptococcus pneumoniae.
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=1313;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TIGR4;
 RX MEDLINE=21357209; PubMed=11463916;
 RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,
 RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,
 RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,
 RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,
 RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,
 RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,
 RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,
 RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;
 RT "Complete genome sequence of a virulent isolate of Streptococcus
 RT pneumoniae.";
 RL Science 293:498-506(2001).

DR EMBL; AE007391; AAK74982.1; -.
DR TIGR; SP0853; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 35 AA; 4276 MW; 6B8813CC028D6C7B CRC64;

Query Match 16.1%; Score 5; DB 16; Length 35;
Best Local Similarity 100.0%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQD 30
|||
Db 30 KKLQD 34

RESULT 8

O24285

ID O24285 PRELIMINARY; PRT; 28 AA.
AC O24285;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE LFY protein (Fragment).
GN LFY.
OS Pinus radiata (Monterey pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
OX NCBI_TaxID=3347;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Vegetative;
RA Izquierdo L.Y., Vergara R.F., Alvarez-Buylla E.R.;
RT "Partial characterization of Pinus radiata meristem identity homolog
RT gene (LFY).";
RL Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U66725; AAB06792.1; -.
FT NON_TER 1 1
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3376 MW; 1736738622B4EE74 CRC64;

Query Match 12.9%; Score 4; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
|||
Db 15 LRKK 18

RESULT 9

Q8GZQ8

ID Q8GZQ8 PRELIMINARY; PRT; 28 AA.
AC Q8GZQ8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE SNF-1 related kinase (Fragment).
GN BKIN12.

OS *Hordeum vulgare* var. *distichum* (Two-rowed barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 OC Triticeae; *Hordeum*.
 OX NCBI_TaxID=112509;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Igri;
 RA Clark J.S.C., Dani M., Barker J.H.A., Halford N.G., Karp A.;
 RT "Bkin12 Promoter Variants - Examples of Functional Biodiversity?";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF448389; AAN76447.1; -.
 KW Kinase.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2950 MW; 853EDC11F6BB2C6C CRC64;

Query Match 12.9%; Score 4; DB 10; Length 28;
 Best Local Similarity 100.0%; Pred. No. 3.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 18 NLGK 21

RESULT 10

Q49148

ID Q49148 PRELIMINARY; PRT; 29 AA.
 AC Q49148;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE PQQ biosynthesis polypeptide.
 GN PQQD.
 OS *Methylobacterium extorquens*.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Methylobacteriaceae; *Methylobacterium*.
 OX NCBI_TaxID=408;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AM1;
 RX MEDLINE=94179111; PubMed=8132470;
 RA Morris C.J., Biville F., Turlin E., Lee E., Ellermann K., Fan W.H.,
 RA Ramamoorthi R., Springer A.L., Lidstrom M.E.;
 RT "Isolation, phenotypic characterization, and complementation analysis
 RT of mutants of *Methylobacterium extorquens* AM1 unable to synthesize
 RT pyrroloquinoline quinone and sequences of pqqD, pqqG, and pqqC.";
 RL J. Bacteriol. 176:1746-1755(1994).
 DR EMBL; L25889; AAA17878.1; -.
 SQ SEQUENCE 29 AA; 3222 MW; B4831562CF76973C CRC64;

Query Match 12.9%; Score 4; DB 2; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||

Db

8 VSEI 11

RESULT 11

Q9UCL2

ID Q9UCL2 PRELIMINARY; PRT; 29 AA.
AC Q9UCL2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Renal intestinal-type alkaline phosphatase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE.
RX MEDLINE=93092315; PubMed=1458595;
RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
RA Hirano K.;
RT "Chemical nature of intestinal-type alkaline phosphatase in human
RT kidney.";
RL Clin. Chem. 38:2539-2542(1992).
DR InterPro; IPR001952; Alk_phosphatase.
DR ProDom; PD001868; Alk_phosphatase; 1.
SQ SEQUENCE 29 AA; 3250 MW; 30501BB7BEEAD8D0 CRC64;

Query Match 12.9%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29

||||

Db 23 KKLQ 26

RESULT 12

Q96PP3

ID Q96PP3 PRELIMINARY; PRT; 29 AA.
AC Q96PP3;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Lympho-epithelial Kazal type-related inhibitor LEKTI (Fragment).
GN SPINK5.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Sprecher E., Chavanas S., DiGiovanna J.J., Amin S., Nielsen K.,
RA Prendiville J.S., Silverman R., Esterly N.B., Spraker M.K., Guelig E.,
RA de Luna M.L., Williams M.L., Buehler B., Pfendner E., Bale S.J.,
RA Uitto J., Hovnanian A., Richard G.;
RT "The spectrum of pathogenic mutations in SPINK 5 in 19 families with
RT Netherton syndrome - Implications for mutation detection and first

RT case of prenatal diagnosis.";
RL J. Invest. Dermatol. 0:0-0(2001).
DR EMBL; AF295783; AAK97140.1; -.
FT NON_TER 1 1
FT NON_TER 29 29
SQ SEQUENCE 29 AA; 3449 MW; 9F31E2AD857EC1BB CRC64;

Query Match 12.9%; Score 4; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
|||
Db 14 NLGK 17

RESULT 13

Q25603

ID Q25603 PRELIMINARY; PRT; 29 AA.
AC Q25603;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Tubulin.
OS Onchocerca volvulus.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Onchocerca.
OX NCBI_TaxID=6282;
RN [1]
RP SEQUENCE FROM N.A.
RA Chandrashekar R., Curtis K.C., Weil G.J.;
RT "Onchocerca volvulus cDNA clone."
RL Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases.
DR EMBL; U15095; AAA50364.1; -.
SQ SEQUENCE 29 AA; 3539 MW; B917126A923EF884 CRC64;

Query Match 12.9%; Score 4; DB 5; Length 29;
Best Local Similarity 100.0%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
|||
Db 4 VSEI 7

RESULT 14

O13043

ID O13043 PRELIMINARY; PRT; 29 AA.
AC O13043;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Whn transcription factor (Fragment).
GN WHN.
OS Scyliorhinus canicula (Spotted dogfish) (Spotted catshark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Galeomorphii; Galeoidea; Carcharhiniformes;

OC Scyliorhinidae; Scyliorhinus.
 OX NCBI_TaxID=7830;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97268658; PubMed=9108066;
 RA Schlake T., Schorpp M., Nehls M., Boehm T.;
 RT "The nude gene encodes a sequence-specific DNA binding protein with
 RT homologs in organisms that lack an anticipatory immune system.";
 RL Proc. Natl. Acad. Sci. U.S.A. 94:3842-3847(1997).
 DR EMBL; Y11539; CAA72302.1; -.
 DR InterPro; IPR001766; TF_Fork_head.
 DR Pfam; PF00250; Fork_head; 1.
 DR ProDom; PD000425; TF_Fork_head; 1.
 FT NON_TER 1 1
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3243 MW; 62AE51F2BE7311E2 CRC64;

Query Match 12.9%; Score 4; DB 13; Length 29;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 17 VSEI 20

RESULT 15

Q9JMV3

ID Q9JMV3 PRELIMINARY; PRT; 30 AA.
 AC Q9JMV3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Luciferase alpha-subunit (Fragment).
 GN LUXA.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB101;
 RA Lotz W., Bauer T.;
 RT "luxAB/kan-cassette for site-directed insertion mutagenesis and
 RT bacterial transcription studies.";
 RL Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB101;
 RA Olsson O., Koncz C., Szalay A.;
 RT "The use of luxA gene of the bacterial luciferase operon as a reporter
 RT gene.";
 RL Mol. Gen. Genet. 215:1-9(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=HB101;
 RX MEDLINE=92114868; PubMed=1685011;

RA Escher A., O'Kane D.J., Szalay A.;
 RT "The beta subunit polypeptide of *Vibrio harveyi* luciferase determines
 RT light emission at 42 degrees C.";
 RL Mol. Gen. Genet. 230:385-393(1991).
 DR EMBL; AJ249443; CAB96206.1; -.
 DR HSSP; P07740; 1LUC.
 DR InterPro; IPR002103; Bac_luciferase.
 DR Pfam; PF00296; bac_luciferase; 1.
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3454 MW; 2FC87235BDBE72FD CRC64;

Query Match 12.9%; Score 4; DB 2; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLGK 13
 ||||
 Db 26 NLGK 29

RESULT 16

Q9UBV5

ID Q9UBV5 PRELIMINARY; PRT; 30 AA.
 AC Q9UBV5;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Intestinal alkaline phosphatase (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=93092315; PubMed=1458595;
 RA Nishihara Y., Hayashi Y., Adachi T., Koyama I., Stigbrand T.,
 RA Hirano K.;
 RT "Chemical nature of intestinal-type alkaline phosphatase in human
 RT kidney.";
 RL Clin. Chem. 38:2539-2542(1992).
 DR InterPro; IPR001952; Alk_phosphatase.
 DR ProDom; PD001868; Alk_phosphatase; 1.
 SQ SEQUENCE 30 AA; 3349 MW; 30501BB7BEB9BDE6 CRC64;

Query Match 12.9%; Score 4; DB 4; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 24 KKLQ 27

RESULT 17

Q8DZP7

ID Q8DZP7 PRELIMINARY; PRT; 30 AA.
 AC Q8DZP7;

DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN SAG1053.
 OS Streptococcus agalactiae (serotype V).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 OC Streptococcus.
 OX NCBI_TaxID=216466;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=2603 V/R / Serotype V;
 RX MEDLINE=22222988; PubMed=12200547;
 RA Tettelin H., Massignani V., Cieslewicz M.J., Eisen J.A., Peterson S.,
 RA Wessels M.R., Paulsen I.T., Nelson K.E., Margarit I., Read T.D.,
 RA Madoff L.C., Wolf A.M., Beanan M.J., Brinkac L.M., Daugherty S.C.,
 RA DeBoy R.T., Durkin A.S., Kolonay J.F., Madupu R., Lewis M.R.,
 RA Radune D., Fedorova N.B., Scanlan D., Khouri H., Mulligan S.,
 RA Carty H.A., Cline R.T., Van Aken S.E., Gill J., Scarselli M., Mora M.,
 RA Iacobini E.T., Brettoni C., Galli G., Mariani M., Vegni F., Maione D.,
 RA Rinaudo D., Rappuoli R., Telford J.L., Kasper D.L., Grandi G.,
 RA Fraser C.M.;
 RT "Complete genome sequence and comparative genomic analysis of an
 RT emerging human pathogen, serotype V Streptococcus agalactiae.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:12391-12396(2002).
 DR EMBL; AE014240; AAM99934.1; -.
 DR TIGR; SAG1053; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 30 AA; 3492 MW; 8BC8F7525007AE91 CRC64;

Query Match 12.9%; Score 4; DB 16; Length 30;
 Best Local Similarity 100.0%; Pred. No. 3.2e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 23 KKLQ 26

RESULT 18

Q55314

ID Q55314 PRELIMINARY; PRT; 31 AA.
 AC Q55314;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Urf2 protein (Fragment).
 GN URF2.
 OS Sulfolobus solfataricus.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OC Sulfolobus.
 OX NCBI_TaxID=2287;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96085144; PubMed=8521845;
 RA Jones C.E., Fleming T.M., Cowan D.A., Littlechild J.A., Piper P.W.;
 RT "The phosphoglycerate kinase and glyceraldehyde-3-phosphate

RT dehydrogenase genes from the thermophilic archaeon Sulfolobus
 RT solfataricus overlap by 8bp. Isolation, sequencing of the genes and
 RT expression on Escherichia coli.";
 RL Eur. J. Biochem. 233:800-808(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94082761; PubMed=8259927;
 RA Arcari P., Russo A.D., Ianniciello G., Gallo M., Bocchini V.;
 RT "Nucleotide sequence and molecular evolution of the gene coding for
 RT glyceraldehyde-3-phosphate dehydrogenase in the thermoacidophilic
 RT archaeobacterium Sulfolobus solfataricus.";
 RL Biochem. Genet. 31:241-251(1993).
 DR EMBL; X80178; CAA56461.1; -.
 FT NON_TER 31 31
 SQ SEQUENCE 31 AA; 3554 MW; 9A2538F911C7309A CRC64;

Query Match 12.9%; Score 4; DB 1; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
 Db 11 WLRK 14

RESULT 19

Q8NEI8

ID Q8NEI8 PRELIMINARY; PRT; 31 AA.
 AC Q8NEI8;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Kidney;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; BC030993; AAH30993.1; -.
 KW Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 31 AA; 3437 MW; 72DCD0761839F7F7 CRC64;

Query Match 12.9%; Score 4; DB 4; Length 31;
 Best Local Similarity 100.0%; Pred. No. 3.3e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSEI 5
 ||||
 Db 18 VSEI 21

RESULT 20

Q9MS77

ID Q9MS77 PRELIMINARY; PRT; 31 AA.
AC Q9MS77;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Photosystem I protein M.
GN PSAM.
OS Phacus acuminata.
OG Chloroplast.
OC Eukaryota; Euglenozoa; Euglenida; Euglenales; Phacus.
OX NCBI_TaxID=130316;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21080550; PubMed=11212923;
RA Doetsch N.A., Thompson M.D., Favreau M.R., Hallick R.B.;
RT "Comparison of psbK operon organization and group III intron content
RT in chloroplast genomes of 12 Euglenoid species.";
RL Mol. Gen. Genet. 264:682-690(2001).
DR EMBL; AF241276; AAF82438.1; -.
KW Chloroplast.
SQ SEQUENCE 31 AA; 3449 MW; 2FFB2AF4B4ACDEC8 CRC64;

Query Match 12.9%; Score 4; DB 8; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLGK 13
|||
Db 24 NLGK 27

RESULT 21

O50669

ID O50669 PRELIMINARY; PRT; 31 AA.
AC O50669;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein BBH11.
GN BBH11.
OS Borrelia burgdorferi (Lyme disease spirochete).
OG Plasmid lp28-3.
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Utterback T., Watthey L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;

RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
RT burgdorferi.";
RL Nature 390:580-586(1997).
DR EMBL; AE000784; AAC66002.1; -.
DR TIGR; BBH11; -.
KW Hypothetical protein; Plasmid; Complete proteome.
SQ SEQUENCE 31 AA; 3892 MW; 8C9F6B9E72D10FBA CRC64;

Query Match 12.9%; Score 4; DB 16; Length 31;
Best Local Similarity 100.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
|||
Db 26 KKLQ 29

RESULT 22

Q9QZQ2

ID Q9QZQ2 PRELIMINARY; PRT; 32 AA.
AC Q9QZQ2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Neurotensin receptor (Fragment).
GN NTSR OR NTR1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=129;
RX MEDLINE=99445567; PubMed=10514493;
RA Tavares D., Tully K., Dobner P.R.;
RT "Sequences required for induction of neurotensin receptor gene
RT expression during neuronal differentiation of N1E-115 neuroblastoma
RT cells.";
RL J. Biol. Chem. 274:30066-30079(1999).
DR EMBL; AF172326; AAD51806.1; -.
DR MGD; MGI:97386; Ntsr.
KW Receptor.
FT NON_TER 32 32
SQ SEQUENCE 32 AA; 3447 MW; 7F7EA4FA2CCF2EFB CRC64;

Query Match 12.9%; Score 4; DB 11; Length 32;
Best Local Similarity 100.0%; Pred. No. 3.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 14 HLNS 17
|||
Db 2 HLNS 5

RESULT 23

Q9HSZ0

ID Q9HSZ0 PRELIMINARY; PRT; 32 AA.

AC Q9HSZ0;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
 DE Vng0019h.
 GN VNG0019H.
 OS Halobacterium sp. (strain NRC-1).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OX NCBI_TaxID=64091;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20504483; PubMed=11016950;
 RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,
 RA Shukla H.D., Lasky S.R., Baliga N.S., Thorsson V., Sbrogna J.,
 RA Swartzell S., Weir D., Hall J., Dahl T.A., Welti R., Goo Y.A.,
 RA Leithauser B., Keller K., Cruz R., Danson M.J., Hough D.W.,
 RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
 RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
 RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,
 RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., DasSarma S.;
 RT "Genome sequence of Halobacterium species NRC-1."
 RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).
 DR EMBL; AE004971; AAG18659.1; -.
 KW Complete proteome.
 SQ SEQUENCE 32 AA; 3758 MW; 22D669246C97A817 CRC64;

 Query Match 12.9%; Score 4; DB 17; Length 32;
 Best Local Similarity 100.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 27 KLQD 30
 ||||
 Db 13 KLQD 16

RESULT 24

Q95SD4

ID Q95SD4 PRELIMINARY; PRT; 33 AA.
 AC Q95SD4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE GM02640p.
 GN BCDNA:GM02640.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nunoo J., Pacleb J., Paragas V., Park S., Phouanenvong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celniker S.;

RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AY060847; AAL28395.1; -.
DR FlyBase; FBgn0047288; BcDNA:GM02640.
SQ SEQUENCE 33 AA; 3720 MW; 9C3FC1AEC9FBE4A7 CRC64;

Query Match 12.9%; Score 4; DB 5; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
|||
Db 21 KKLQ 24

RESULT 25

Q9PKX3

ID Q9PKX3 PRELIMINARY; PRT; 33 AA.
AC Q9PKX3;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein TC0337.
GN TC0337.
OS Chlamydia muridarum.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=83560;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MoPn / Nigg;
RX MEDLINE=20150255; PubMed=10684935;
RA Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg J.F.,
RA White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass S.,
RA Linher K., Weidman J., Khouri H., Craven B., Bowman C., Dodson R.,
RA Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg S.L.,
RA Eisen J., Fraser C.M.;
RT "Genome sequences of Chlamydia trachomatis MoPn and Chlamydia
RT pneumoniae AR39.";
RL Nucleic Acids Res. 28:1397-1406(2000).
DR EMBL; AE002301; AAF39200.1; -.
DR TIGR; TC0337; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 33 AA; 4075 MW; 1E7C5AD9BA5371EC CRC64;

Query Match 12.9%; Score 4; DB 16; Length 33;
Best Local Similarity 100.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 LRKK 27
|||
Db 26 LRKK 29

RESULT 26

Q9ZG81

ID Q9ZG81 PRELIMINARY; PRT; 34 AA.
AC Q9ZG81;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)

DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
 DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
 DE ATP-dependent permease (Fragment).
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_TaxID=813;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=L2 434B;
 RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
 RT "Gene identification of Chlamydia trachomatis by random DNA
 RT sequencing.";
 RL Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF087260; AAD04038.1; -.
 FT NON_TER 1 1
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 4186 MW; 3B38196393258A53 CRC64;

Query Match 12.9%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
 ||||
 Db 25 LRKK 28

RESULT 27

Q8GFK2

ID Q8GFK2 PRELIMINARY; PRT; 34 AA.
 AC Q8GFK2;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ORF37.
 OS Staphylococcus aureus.
 OG Plasmid EDINA plasmid.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=E-1;
 RA Sugai M., Yamaguchi T., Hayashi T., Nakasone K., Takami H.;
 RT "Complete nucleotide sequence of Staphylococcus aureus E-1 EDINA
 RT plasmid.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AP003089; BAC54529.1; -.
 KW Plasmid.
 SQ SEQUENCE 34 AA; 4138 MW; 88FBD773858BC6EE CRC64;

Query Match 12.9%; Score 4; DB 2; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKLQ 29
 ||||
 Db 6 KKLQ 9

RESULT 28

Q8C4P4

ID Q8C4P4 PRELIMINARY; PRT; 34 AA.
 AC Q8C4P4;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Zinc finger homeodomain 4 (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Head;
 RX MEDLINE=22354683; PubMed=12466851;
 RA The FANTOM Consortium,
 RA the RIKEN Genome Exploration Research Group Phase I & II Team;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 DR EMBL; AK081561; BAC38260.1; -.
 FT NON_TER 1 1
 SQ SEQUENCE 34 AA; 3755 MW; EF41DCAF348467B0 CRC64;

Query Match 12.9%; Score 4; DB 11; Length 34;
 Best Local Similarity 100.0%; Pred. No. 3.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
 ||||
 Db 2 KLQD 5

RESULT 29

Q90ZJ4

ID Q90ZJ4 PRELIMINARY; PRT; 34 AA.
 AC Q90ZJ4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Platelet-derived growth factor A chain long form (Fragment).
 GN PDGF-A.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21363439; PubMed=11470524;
 RA Horiuchi H., Inoue T., Furusawa S., Matsuda H.;
 RT "Characterization and expression of three forms of cDNA encoding
 RT chicken platelet-derived growth factor-A chain."
 RL Gene 272:181-190(2001).

DR EMBL; AB031024; BAB62544.1; -.
FT NON_TER 1 1
SQ SEQUENCE 34 AA; 3983 MW; FEF02F8A45B27DA5 CRC64;

Query Match 12.9%; Score 4; DB 13; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKKL 28
|||
Db 28 RKKL 31

RESULT 30

Q98FK5

ID Q98FK5 PRELIMINARY; PRT; 34 AA.
AC Q98FK5;
DT 01-OCT-2001 (TrEMBLrel. 18, Created)
DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein msr3733.
GN MSR3733.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti.";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003002; BAB50562.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 34 AA; 3804 MW; D6AAA82ECB590413 CRC64;

Query Match 12.9%; Score 4; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 27 KLQD 30
|||
Db 28 KLQD 31

RESULT 31

Q8G2Q2

ID Q8G2Q2 PRELIMINARY; PRT; 34 AA.
AC Q8G2Q2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Hypothetical protein.
GN BR0266.
OS Brucella suis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=29461;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1330 / Biovar 1;
RX MEDLINE=22247741; PubMed=12271122;
RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
RA Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
RA Daugherty S.C., Deboy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
RA Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
RA Riedmuller S., Tettelin H., Gill S.R., White O., Salzberg S.L.,
RA Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.;
RT "The Brucella suis genome reveals fundamental similarities between
RT animal and plant pathogens and symbionts.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
DR EMBL; AE014339; AAN29215.1; -.
DR TIGR; BR0266; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 34 AA; 3781 MW; 76E820326E6CA66E CRC64;

Query Match 12.9%; Score 4; DB 16; Length 34;
Best Local Similarity 100.0%; Pred. No. 3.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGKH 14
|||
Db 10 LGKH 13

RESULT 32

Q15421
ID Q15421 PRELIMINARY; PRT; 35 AA.
AC Q15421;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Simian sarcoma associated virus (SSAV)-related pol region DNA
DE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87071681; PubMed=2431542;
RA Leib-Mosch C., Brack R., Werner T., Erfle V., Hehlmann R.;
RT "Isolation of an SSAV-related endogenous sequence from Human DNA.";
RL Virology 155:666-677(1986).
DR EMBL; M14911; AAA36592.1; -.
FT NON_TER 1 1
FT NON_TER 35 35
SQ SEQUENCE 35 AA; 3742 MW; 2F70B02EE0BC86DF CRC64;

Query Match 12.9%; Score 4; DB 4; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
 ||||
Db 6 LQDV 9

RESULT 33

Q8V6J8

ID Q8V6J8 PRELIMINARY; PRT; 35 AA.
AC Q8V6J8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical 4.1 kDa protein.
OS Halovirus HF2.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
OX NCBI_TaxID=33771;
RN [1]
RP SEQUENCE FROM N.A.
RA Tang S.-L., Fisher C., Ngui K., Nuttall S.D., Dyal-Smith M.L.;
RT "Sequence and transcription of halovirus HF2."
RL Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL; AF222060; AAL55025.1; -.
KW Hypothetical protein.
SQ SEQUENCE 35 AA; 4115 MW; 2652C319622E9CE4 CRC64;

Query Match 12.9%; Score 4; DB 12; Length 35;
Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSE 4
 ||||
Db 10 SVSE 13

RESULT 34

Q9KQG4

ID Q9KQG4 PRELIMINARY; PRT; 35 AA.
AC Q9KQG4;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Hypothetical protein VC2034.
GN VC2034.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,

RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
 RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
 RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
 RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
 RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
 RA Fraser C.M.;
 RT "DNA sequence of both chromosomes of the cholera pathogen *Vibrio*
 RT *cholerae*.";
 RL Nature 406:477-483(2000).
 DR EMBL; AE004278; AAF95182.1; -.
 DR TIGR; VC2034; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4181 MW; D185B6339A711D54 CRC64;

Query Match 12.9%; Score 4; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
 ||||
 Db 24 KKLQ 27

RESULT 35

Q8F102

ID Q8F102 PRELIMINARY; PRT; 35 AA.
 AC Q8F102;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 GN LA3339.
 OS *Leptospira interrogans*.
 OC Bacteria; Spirochaetes; Spirochaetales; Leptosiraceae; *Leptospira*.
 OX NCBI_TaxID=173;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=56601 / Serogroup Icterohaemorrhagiae / Serovar lai;
 RA Ren S.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE011494; AAN50536.1; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 35 AA; 4253 MW; 0DDFEDFFB32E980B CRC64;

Query Match 12.9%; Score 4; DB 16; Length 35;
 Best Local Similarity 100.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 HLNS 17
 ||||
 Db 3 HLNS 6

RESULT 36

Q53920

ID Q53920 PRELIMINARY; PRT; 36 AA.
 AC Q53920;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE OrfA protein (Fragment).
 GN ORFA.
 OS Streptomyces chrysomallus.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1899;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94341259; PubMed=8062824;
 RA Pahl A., Keller U.;
 RT "Streptomyces chrysomallus FKBP-33 is a novel immunophilin consisting
 RT of two FK506-binding domains with its gene transcriptionally coupled
 RT to the FKBP-12 gene."
 RL EMBO J. 13:3472-3480(1994).
 DR EMBL; Z34523; CAA84281.1; -.
 DR InterPro; IPR004347; DUF245.
 DR Pfam; PF03136; DUF245; 1.
 FT NON_TER 1 1
 SQ SEQUENCE 36 AA; 4121 MW; EBD470AAF99A728E CRC64;

Query Match 12.9%; Score 4; DB 2; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERVE 22
 ||||
 Db 27 ERVE 30

RESULT 37

O68941

ID O68941 PRELIMINARY; PRT; 36 AA.
 AC O68941;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Dinitrogenase 3 beta subunit (Fragment).
 GN ANFK.
 OS Rhodospirillum rubrum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhodospirillales;
 OC Rhodospirillaceae; Rhodospirillum.
 OX NCBI_TaxID=1085;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Loveless T.M., Bishop P.E.;
 RT "Identification of Genes Unique to Mo-Independent Nitrogenase Systems
 RT in Diverse Diazotrophs."
 RL Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AF058778; AAC14327.1; -.
 DR InterPro; IPR000510; Oxred_nitrognasel.
 DR Pfam; PF00148; oxidored_nitro; 1.
 FT NON_TER 36 36
 SQ SEQUENCE 36 AA; 3957 MW; D94F46BCFD437D97 CRC64;

Query Match 12.9%; Score 4; DB 2; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 LRKK 27
||||
Db 5 LRKK 8

RESULT 38

Q8WXW8

ID Q8WXW8 PRELIMINARY; PRT; 36 AA.
AC Q8WXW8;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Urea transporter JK glycoprotein (Fragment).
GN JK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Olsson M.L., Irshaid N.M., Eicher N.I., Poole J., Hustinx H.;
RT "Molecular Basis of the Jk(a-b-) Phenotype in Non-Finnish European
RT Pedigrees.";
RL Br. J. Haematol. 0:0-0(2001).
DR EMBL; AF328890; AAL37474.1; -.
DR InterPro; IPR004937; Urea_transporter.
DR Pfam; PF03253; UT; 1.
FT NON_TER 1 1
SQ SEQUENCE 36 AA; 3989 MW; C3A6A964C2F41007 CRC64;

Query Match 12.9%; Score 4; DB 4; Length 36;
Best Local Similarity 100.0%; Pred. No. 3.8e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNSM 18
||||
Db 7 LNSM 10

RESULT 39

Q9SJ63

ID Q9SJ63 PRELIMINARY; PRT; 36 AA.
AC Q9SJ63;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE At2g35870 protein.
GN AT2G35870.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
 RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
 RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
 RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
 RA Salzberg S.L., Fraser C.M., Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana.";
 RL Nature 402:761-768(1999).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;
 RA Lin X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AC007017; AAD21470.1; -.
 SQ SEQUENCE 36 AA; 4358 MW; DC966779BBD6B834 CRC64;

Query Match 12.9%; Score 4; DB 10; Length 36;
 Best Local Similarity 100.0%; Pred. No. 3.8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 26 KKLQ 29
 ||||
 Db 4 KKLQ 7

RESULT 40

Q9PXD1

ID Q9PXD1 PRELIMINARY; PRT; 36 AA.
 AC Q9PXD1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Genome polyprotein [Contains: envelope glycoprotein E2/NS1 (GP68)]
 DE (Fragment).
 OS Hepatitis C virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Hepacivirus.
 OX NCBI_TaxID=11103;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96343121; PubMed=8750162;
 RA Chayama K., Tsubota A., Arase Y., Saitoh S., Ikeda K., Matsumoto T.,
 RA Hashimoto M., Kobayashi M., Kanda M., Morinaga T.;
 RT "Genotype, slow decrease in virus titer during interferon treatment
 RT and high degree of sequence variability of hypervariable region are
 RT indicative of poor response to interferon treatment in patients with
 RT chronic hepatitis type C.";
 RL J. Hepatol. 23:648-653(1995).
 DR InterPro; IPR002531; HCV_NS1.
 DR Pfam; PF01560; HCV_NS1; 1.
 KW Coat protein; Envelope protein; Glycoprotein; Nonstructural protein;

KW Polyprotein; Transmembrane.

SQ SEQUENCE 36 AA; 3546 MW; 5BB7935A55048D34 CRC64;

Query Match 12.9%; Score 4; DB 12; Length 36;

Best Local Similarity 100.0%; Pred. No. 3.8e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQLM 8

||||

Db 33 IQLM 36

Search completed: January 14, 2004, 10:41:56

Job time : 25.1776 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 14, 2004, 10:28:19 ; Search time 5.11838 Seconds
(without alignments)
284.822 Million cell updates/sec

Title: US-09-843-221A-165
Perfect score: 31
Sequence: 1 SVSEIQLMHNLGKHLNSMERVEWLRKKLQDV 31

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1319

Minimum DB seq length: 28
Maximum DB seq length: 40

Post-processing: Listing first 1000 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	5	16.1	33	1	FABI_RHASA	P81175 rhamdia sap
2	4	12.9	29	1	DMD_RAT	P11530 rattus norv
3	4	12.9	39	1	PSBY_SYNY3	P73676 synechocyst
4	4	12.9	39	1	SR1C_SARPE	P08377 sarcophaga
5	3	9.7	28	1	CH60_MYCSM	P80673 mycobacteri
6	3	9.7	28	1	COXB_SOLTU	P80499 solanum tub
7	3	9.7	28	1	GUN_SCHCO	P81190 schizophyll
8	3	9.7	28	1	PA23_TRIST	P82894 trimeresuru
9	3	9.7	28	1	PA2C_PSEPO	P20260 pseudechis
10	3	9.7	28	1	VI03_VACCP	Q00334 vaccinia vi
11	3	9.7	28	1	VIP_ALLMI	P48142 alligator m
12	3	9.7	28	1	VIP_RANRI	P81016 rana ridibu
13	3	9.7	28	1	VIP_SHEEP	P04565 ovis aries
14	3	9.7	29	1	GALA_ALLMI	P47215 alligator m
15	3	9.7	29	1	GALA_AMICA	P47214 amia calva
16	3	9.7	29	1	GALA_CHICK	P30802 gallus gall
17	3	9.7	29	1	GALA_ONCMY	P47213 oncorhynchu

18	3	9.7	29	1	GALA_RANRI	P47216	rana ridibu
19	3	9.7	29	1	GALA_SHEEP	P31234	ovis aries
20	3	9.7	29	1	GLUC_CHIBR	P31297	chinchilla
21	3	9.7	29	1	IPYR_DESVH	P19371	desulfovibr
22	3	9.7	29	1	NUO1_SOLTU	P80267	solanum tub
23	3	9.7	29	1	P2SM_LOXIN	P83046	loxosceles
24	3	9.7	29	1	PCG4_PACGO	P82417	pachycondyl
25	3	9.7	29	1	RS7_METTE	O93639	methanosarc
26	3	9.7	29	1	SODC_OLEEU	P80740	olea europa
27	3	9.7	29	1	TL16_SPIOL	P81834	spinacia ol
28	3	9.7	30	1	DMS3_PHYSA	P80279	phyllomedus
29	3	9.7	30	1	FTN_BACFR	P28733	bacteroides
30	3	9.7	30	1	GLUM_ANGAN	P41521	anguilla an
31	3	9.7	30	1	OTCC_AERPU	P11726	aeromonas p
32	3	9.7	30	1	PCG2_PACGO	P82415	pachycondyl
33	3	9.7	30	1	PCG3_PACGO	P82416	pachycondyl
34	3	9.7	30	1	PSAM_PORPU	P51395	porphyra pu
35	3	9.7	30	1	TX2_THRPR	P83476	thrixopelma
36	3	9.7	30	1	UP61_UPEIN	P82037	uperoleia i
37	3	9.7	30	1	UP62_UPEIN	P82038	uperoleia i
38	3	9.7	30	1	VAA2_EQUAR	Q04238	equisetum a
39	3	9.7	30	1	Y523_BORBU	O51473	borrelia bu
40	3	9.7	31	1	CEC1_PIG	P14661	sus scrofa
41	3	9.7	31	1	CXMA_CONMR	P56708	conus marmo
42	3	9.7	31	1	DEJP_DROME	P81160	drosophila
43	3	9.7	31	1	DIUX_DIPPU	P82372	diploptera
44	3	9.7	31	1	H13_WHEAT	P15872	triticum ae
45	3	9.7	31	1	LPL_BUCRP	Q53017	buchnera ap
46	3	9.7	31	1	MALK_PHOLU	P41124	photorhabdu
47	3	9.7	31	1	NAP4_HUMAN	P19877	homo sapien
48	3	9.7	31	1	PETL_LOTJA	Q9bbr4	lotus japon
49	3	9.7	31	1	PETL_MARPO	P12179	marchantia
50	3	9.7	31	1	PETL_MESVI	Q9mun4	mesostigma
51	3	9.7	31	1	PETL_NEPOL	Q9tky9	nephroselmi
52	3	9.7	31	1	PSAM_EUGGR	P31479	euglena gra
53	3	9.7	31	1	SARL_MOUSE	Q9cqd6	mus musculu
54	3	9.7	31	1	SARL_RABIT	P42532	oryctolagus
55	3	9.7	31	1	SCK5_ANDMA	P31719	androctonus
56	3	9.7	31	1	SCKL_LEIQH	P16341	leiurus qui
57	3	9.7	31	1	Y822_BORBU	O51762	borrelia bu
58	3	9.7	32	1	ADHR_DROYA	P28487	drosophila
59	3	9.7	32	1	CAL2_ONCKE	P01264	oncorhynchu
60	3	9.7	32	1	CAL3_ONCKI	P01265	oncorhynchu
61	3	9.7	32	1	CAL_ANGJA	P01262	anguilla ja
62	3	9.7	32	1	COA2_BPIF1	O80296	bacterioph
63	3	9.7	32	1	CY31_DESAC	P81078	desulfuromo
64	3	9.7	32	1	FF21_SALEN	P55224	salmonella
65	3	9.7	32	1	IAPP_PIG	Q29119	sus scrofa
66	3	9.7	32	1	ITR3_CUCPE	P10293	cucurbita p
67	3	9.7	32	1	ITR4_CUCMA	P07853	cucurbita m
68	3	9.7	32	1	LEC_DOLAX	P02875	dolichos ax
69	3	9.7	32	1	MIFH_TRITR	P81748	trichuris t
70	3	9.7	32	1	P1SM_LOXIN	P83045	loxosceles
71	3	9.7	32	1	PETM_GUITH	O78499	guillardia
72	3	9.7	32	1	PHSS_DESBN	P13064	desulfovibr
73	3	9.7	32	1	PSAM_MARPO	P31590	marchantia
74	3	9.7	32	1	PSBQ_PEA	P19589	pisum sativ

75	3	9.7	32	1	PSBT_ODOSI	P49516	odontella s
76	3	9.7	32	1	PSBZ_EUGST	Q8sl89	euglena ste
77	3	9.7	32	1	PSBZ_EUGVI	Q8sl87	euglena vir
78	3	9.7	32	1	Y16O_BPT4	P39247	bacterioph
79	3	9.7	32	1	YCPG_MASLA	P29735	mastigoclad
80	3	9.7	33	1	GGN1_RANRU	P80395	rana rugosa
81	3	9.7	33	1	GLU2_ORENI	P81027	oreochromis
82	3	9.7	33	1	RUGB_RANRU	P80955	rana rugosa
83	3	9.7	33	1	T1F_PARTE	Q27172	paramecium
84	3	9.7	33	1	Y50A_MYCTU	Q9cb56	mycobacteri
85	3	9.7	33	1	YC12_EUGGR	P31559	euglena gra
86	3	9.7	34	1	DMS1_PHYSA	P24302	phyllomedus
87	3	9.7	34	1	DMS2_PHYSA	P80278	phyllomedus
88	3	9.7	34	1	GAST_CAPHI	P04564	capra hircu
89	3	9.7	34	1	GUN1_SCLSC	P21833	sclerotinia
90	3	9.7	34	1	TX1_SCOGR	P56855	scodra gris
91	3	9.7	35	1	CECA_AEDAL	P81417	aedes albop
92	3	9.7	35	1	COPA_CANFA	P40765	canis famil
93	3	9.7	35	1	CPI2_PIG	P80736	sus scrofa
94	3	9.7	35	1	GP58_BPSP1	O48412	bacterioph
95	3	9.7	35	1	LEC1_CYTSE	P22970	cytisis ses
96	3	9.7	35	1	LEC3_ULEEU	P23032	ulex europe
97	3	9.7	35	1	NP30_STAAU	P21222	staphylococ
98	3	9.7	35	1	PBP_ORGPS	P34178	orgyia pseu
99	3	9.7	35	1	PETG_CYACA	Q9tlq9	cyanidium c
100	3	9.7	35	1	PSBM_SYNY3	P72701	synechocyst
101	3	9.7	35	1	RL15_SYNP7	P31160	synechococc
102	3	9.7	35	1	SCKK_TITSE	P56219	tityus serr
103	3	9.7	35	1	TX1_GRASP	P56852	grammostola
104	3	9.7	35	1	TX1_THRPR	P83480	thrixopelma
105	3	9.7	35	1	TX2_GRASP	P56853	grammostola
106	3	9.7	35	1	VORB_METTM	P80908	methanobact
107	3	9.7	35	1	YRKM_BACSU	P54440	bacillus su
108	3	9.7	36	1	ELH_THETS	P80594	theromyzon
109	3	9.7	36	1	NPF_ARTTR	P41334	artioposthi
110	3	9.7	36	1	OSTS_YEAST	Q99380	saccharomyc
111	3	9.7	36	1	PETM_SYNY3	P74810	synechocyst
112	3	9.7	36	1	R18A_BOVIN	P82919	bos taurus
113	3	9.7	36	1	RET4_CHICK	P30370	gallus gall
114	3	9.7	36	1	RL6_HALCU	P05968	halobacteri
115	3	9.7	36	1	Y260_BACHD	Q9kg53	bacillus ha
116	3	9.7	36	1	Y609_ARCFU	O29646	archaeoglob
117	3	9.7	37	1	DIU1_TENMO	P56618	tenebrio mo
118	3	9.7	37	1	IAPP_CRIGR	P19890	cricetulus
119	3	9.7	37	1	LCNM_LACLA	P83002	lactococcus
120	3	9.7	37	1	OGT1_RABIT	P81436	oryctolagus
121	3	9.7	37	1	PIP7_BOVIN	P21671	bos taurus
122	3	9.7	37	1	RL36_PASMU	P57942	pasteurella
123	3	9.7	37	1	SCKI_MESTA	P24663	mesobuthus
124	3	9.7	37	1	Y63_BPT3	P20328	bacterioph
125	3	9.7	38	1	CPRP_CANPG	P81033	cancer pagu
126	3	9.7	38	1	DNP_DENAN	P28374	dendroaspis
127	3	9.7	38	1	NLT1_VITSX	P80275	vitis sp. (
128	3	9.7	38	1	NLT2_VITSX	P33556	vitis sp. (
129	3	9.7	38	1	OBP2_HYSCR	P81648	hystrix cri
130	3	9.7	38	1	PYSA_METBA	P80521	methanosarc
131	3	9.7	38	1	RL36_ECOLI	P21194	escherichia

132	3	9.7	38	1	RL36_PSEAE	Q9hwf6	pseudomonas
133	3	9.7	38	1	RL36_THEMA	Q9x1i6	thermotoga
134	3	9.7	38	1	RL36_YERPE	Q8zj91	yersinia pe
135	3	9.7	38	1	RR12_PINCO	P49168	pinus conto
136	3	9.7	38	1	YJ39_ARCFU	O28340	archaeoglob
137	3	9.7	39	1	CEC_GLOMR	P83403	glossina mo
138	3	9.7	39	1	COLI_BALPH	P01195	balaenopter
139	3	9.7	39	1	COLI_RABIT	P06297	oryctolagus
140	3	9.7	39	1	COLI_SQUAC	P01197	squalus aca
141	3	9.7	39	1	COLI_STRCA	P01196	struthio ca
142	3	9.7	39	1	EXE3_HELHO	P20394	heloderma h
143	3	9.7	39	1	FUC3_RAT	P80349	rattus norv
144	3	9.7	39	1	GVPC_SPICC	P81000	spirulina s
145	3	9.7	39	1	H2A_BUFBG	P55897	bufo bufo g
146	3	9.7	39	1	LCGA_LACLA	P36961	lactococcus
147	3	9.7	39	1	PA2_AGKBI	Q9psf9	agkistrodon
148	3	9.7	39	1	PSBX_PORPU	P51197	porphyra pu
149	3	9.7	40	1	ALB1_TRASC	P81188	trachemys s
150	3	9.7	40	1	HPT_RABIT	P19007	oryctolagus
151	3	9.7	40	1	HS9A_RABIT	P30946	oryctolagus
152	3	9.7	40	1	KAD_STACA	P35141	staphylococ
153	3	9.7	40	1	PHRK_BACSU	O31840	bacillus su
154	3	9.7	40	1	PRE_BACLI	P18189	bacillus li
155	3	9.7	40	1	RK33_PEA	P51416	pisum sativ
156	3	9.7	40	1	RRPO_LSV	P27328	lily sympto
157	3	9.7	40	1	SAUV_PHYSA	P01144	phyllomedus
158	3	9.7	40	1	SR1D_SARPE	P18312	sarcophaga
159	3	9.7	40	1	UC11_MAIZE	P80617	zea mays (m
160	3	9.7	40	1	VIT_MELGA	P56531	meleagris g
161	3	9.7	40	1	YDRB_STRPE	P32012	streptomyce
162	2	6.5	28	1	ACON_CANAL	P82611	candida alb
163	2	6.5	28	1	APC1_RABIT	P33047	oryctolagus
164	2	6.5	28	1	ARYC_NOCGL	P80008	nocardia gl
165	2	6.5	28	1	C1QC_RAT	P31722	rattus norv
166	2	6.5	28	1	ETX2_BACCE	P80568	bacillus ce
167	2	6.5	28	1	FIBA_CANFA	P02673	canis famil
168	2	6.5	28	1	FLA1_TREPH	P21988	treponema p
169	2	6.5	28	1	GDO_TRIMO	P02865	triticum mo
170	2	6.5	28	1	GRP_ALLMI	P31886	alligator m
171	2	6.5	28	1	GTS5_CHICK	P20137	gallus gall
172	2	6.5	28	1	GVPC_OSCAG	P80999	oscillatori
173	2	6.5	28	1	HORC_HORSP	P02864	hordeum spo
174	2	6.5	28	1	ICPP_VIPLE	P82475	vipera lebe
175	2	6.5	28	1	IEL1_MOMCH	P10296	momordica c
176	2	6.5	28	1	IORB_METTM	P80911	methanobact
177	2	6.5	28	1	ITR2_MOMCH	P10295	momordica c
178	2	6.5	28	1	ITR3_LUFCY	P35628	luffa cylin
179	2	6.5	28	1	ITRA_MOMCH	P30709	momordica c
180	2	6.5	28	1	LECA_IRIHO	P36230	iris hollan
181	2	6.5	28	1	LPFS_ECOLI	P22183	escherichia
182	2	6.5	28	1	LPL_ECOLI	P09149	escherichia
183	2	6.5	28	1	LPL_SALTI	Q8z9h9	salmonella
184	2	6.5	28	1	LPL_SALTY	P03062	salmonella
185	2	6.5	28	1	LPW_SERMA	P03055	serratia ma
186	2	6.5	28	1	MAAI_RAT	P57113	rattus norv
187	2	6.5	28	1	MCDP_MEGPE	P04567	megabombus
188	2	6.5	28	1	NLT2_WHEAT	P39085	triticum ae

189	2	6.5	28	1	NXL1_BOUAN	P34074	boulengerin
190	2	6.5	28	1	OBP1_HYSCR	P81647	hystrix cri
191	2	6.5	28	1	OMPA_YERPS	P38399	yersinia ps
192	2	6.5	28	1	ORND_PLAOR	P25513	placobdella
193	2	6.5	28	1	OST1_CHICK	P80896	gallus gall
194	2	6.5	28	1	PA22_MICNI	P21791	micrurus ni
195	2	6.5	28	1	PA23_MICNI	P21792	micrurus ni
196	2	6.5	28	1	PETL_CYAPA	P48102	cyanophora
197	2	6.5	28	1	PHR_METTM	P58818	methanobact
198	2	6.5	28	1	PHYB_ASPTI	P81440	aspergillus
199	2	6.5	28	1	PP71_HCMVT	P24429	human cytom
200	2	6.5	28	1	PPOX_BOVIN	P56602	bos taurus
201	2	6.5	28	1	RL5_HALCU	P05972	halobacteri
202	2	6.5	28	1	RS19_PHYS1	O66093	phytoplasma
203	2	6.5	28	1	SCX2_BUTSI	P15230	buthus sind
204	2	6.5	28	1	SLP1_LEIQH	P80669	leiurus qui
205	2	6.5	28	1	SMS2_ORENI	P81029	oreochromis
206	2	6.5	28	1	TXO2_AGEAP	P15971	agelenopsis
207	2	6.5	28	1	VG9_SPV4	P11341	spiroplasma
208	2	6.5	28	1	VIP_DIDMA	P39089	didelphis m
209	2	6.5	28	1	VIP_SCYCA	P09685	scyliorhinu
210	2	6.5	28	1	Y073_ARCFU	O30163	archaeoglob
211	2	6.5	28	1	Y16P_BPT4	P39248	bacterioph
212	2	6.5	28	1	YA79_ARCFU	O29184	archaeoglob
213	2	6.5	29	1	12AH_CLOS4	P21215	clostridium
214	2	6.5	29	1	AL21_HORSE	P81216	equus cabal
215	2	6.5	29	1	ATP9_PICPJ	Q06838	pichia pijp
216	2	6.5	29	1	ATPA_BRYMA	P26965	bryopsis ma
217	2	6.5	29	1	BR2D_RANES	P40840	rana escule
218	2	6.5	29	1	BREE_RANES	P40841	rana escule
219	2	6.5	29	1	CERB_CERCA	P36191	ceratitis c
220	2	6.5	29	1	COA1_BPI22	P15413	bacterioph
221	2	6.5	29	1	COXJ_CANFA	Q9tr29	canis famil
222	2	6.5	29	1	COXK_SHEEP	Q9tr28	ovis aries
223	2	6.5	29	1	CU36_LOCFI	P11737	locusta mig
224	2	6.5	29	1	CXD6_CONGL	Q9twm7	conus glori
225	2	6.5	29	1	CXOC_CONMA	P37300	conus magus
226	2	6.5	29	1	CXOD_CONMA	Q26350	conus magus
227	2	6.5	29	1	CXST_CONGE	P58844	conus geogr
228	2	6.5	29	1	DMS5_PHYSA	P80281	phyllomedus
229	2	6.5	29	1	GLUC_ANAPL	P01276	anas platyr
230	2	6.5	29	1	GLUC_CALMI	P13189	callorhynch
231	2	6.5	29	1	GLUC_DIDMA	P18108	didelphis m
232	2	6.5	29	1	GLUC_LAMFL	Q9prq9	lampetra fl
233	2	6.5	29	1	GLUC_PLAFE	P23062	platichthys
234	2	6.5	29	1	GLUC_RABIT	P25449	oryctolagus
235	2	6.5	29	1	GLUC_TORMA	P09567	torpedo mar
236	2	6.5	29	1	H2B2_ECHES	P13282	echinus esc
237	2	6.5	29	1	HOXY_RHOOP	P22660	rhodococcus
238	2	6.5	29	1	HRJ_BOTJA	P20416	bothrops ja
239	2	6.5	29	1	HS98_NEUCR	P31540	neurospora
240	2	6.5	29	1	ITH3_BOVIN	P56652	bos taurus
241	2	6.5	29	1	ITR1_CUCMA	P01074	cucurbita m
242	2	6.5	29	1	ITR1_LUFCY	P25849	luffa cylin
243	2	6.5	29	1	ITR1_MOMRE	P17680	momordica r
244	2	6.5	29	1	ITR2_BRYDI	P11968	bryonia dio
245	2	6.5	29	1	ITR3_CYCPE	P83394	cyclanthera

246	2	6.5	29	1	ITR4_CYCPE	P83395	cyclanthera
247	2	6.5	29	1	ITR5_CYCPE	P83396	cyclanthera
248	2	6.5	29	1	KDPF_ECOLI	P36937	escherichia
249	2	6.5	29	1	MDH_BURPS	P80536	burkholderi
250	2	6.5	29	1	MULR_ECHML	P81798	echis multi
251	2	6.5	29	1	PETN_ANASP	Q913p6	anabaena sp
252	2	6.5	29	1	PETN_ARATH	P12178	arabidopsis
253	2	6.5	29	1	PETN_CHAGL	Q8ma13	chaetosphae
254	2	6.5	29	1	PETN_CYAPA	P48258	cyanophora
255	2	6.5	29	1	PETN_GUITH	O78498	guillardia
256	2	6.5	29	1	PETN_MAIZE	Q33302	zea mays (m
257	2	6.5	29	1	PETN_MARPO	P12177	marchantia
258	2	6.5	29	1	PETN_MESVI	Q9mus4	mesostigma
259	2	6.5	29	1	PETN_ODOSI	P49527	odontella s
260	2	6.5	29	1	PETN_PINTH	P41611	pinus thunb
261	2	6.5	29	1	PETN_PORPU	P51276	porphyra pu
262	2	6.5	29	1	PETN_PSINU	Q8wi23	psilotum nu
263	2	6.5	29	1	PETN_SKECO	O96807	skeletonema
264	2	6.5	29	1	PETN_SYNEL	Q8dkn2	synechococc
265	2	6.5	29	1	PETN_SYNY3	P72717	synechocyst
266	2	6.5	29	1	PK4_DICDI	P34103	dictyosteli
267	2	6.5	29	1	PRO1_DACGL	P18689	dactylis gl
268	2	6.5	29	1	PSAF_SYNP6	P31083	synechococc
269	2	6.5	29	1	PSAK_SPIOL	P14627	spinacia ol
270	2	6.5	29	1	PSAM_GUITH	O78448	guillardia
271	2	6.5	29	1	PSBI_SYNVU	P12240	synechococc
272	2	6.5	29	1	RL15_HALCU	P05971	halobacteri
273	2	6.5	29	1	RL15_STRLI	P49975	streptomyce
274	2	6.5	29	1	RP54_CLOKL	P38944	clostridium
275	2	6.5	29	1	SCX1_ANDMA	P56215	androctonus
276	2	6.5	29	1	SDHB_CLOPR	P80213	clostridium
277	2	6.5	29	1	SLP2_LEIQH	P80670	leiurus qui
278	2	6.5	29	1	SLP3_LEIQH	P80671	leiurus qui
279	2	6.5	29	1	TAT_HV1Z3	P12510	human immun
280	2	6.5	29	1	TLP_ACTDE	P81370	actinidia d
281	2	6.5	29	1	VARF_VIOAR	P58451	viola arven
282	2	6.5	29	1	Y15_BPT7	P03792	bacterioph
283	2	6.5	29	1	Y51_BPT3	P20326	bacterioph
284	2	6.5	29	1	YCX4_ODOSI	P49830	odontella s
285	2	6.5	29	1	YXCX_ODOSI	P49838	odontella s
286	2	6.5	30	1	2ENR_CLOTY	P11887	clostridium
287	2	6.5	30	1	A1AT_CHIVI	P38026	chinchilla
288	2	6.5	30	1	AATC_RABIT	P12343	oryctolagus
289	2	6.5	30	1	AATM_RABIT	P12345	oryctolagus
290	2	6.5	30	1	ACB1_DIGLA	P81624	digitalis l
291	2	6.5	30	1	AMPT_BACST	P00728	bacillus st
292	2	6.5	30	1	ANF_RANRI	P09196	rana ridibu
293	2	6.5	30	1	CALM_LYTPI	P05935	lytechinus
294	2	6.5	30	1	CBAL_BACST	P13722	bacillus st
295	2	6.5	30	1	CH60_CLOPA	P81339	clostridium
296	2	6.5	30	1	CIRA_CHAPA	P56871	chassalia p
297	2	6.5	30	1	CLPA_PINPS	P81671	pinus pinas
298	2	6.5	30	1	COAE_CORAM	P58101	corynebacte
299	2	6.5	30	1	COXC_SOLTU	P80500	solanum tub
300	2	6.5	30	1	CRG2_SCOWA	P19865	scoliodon w
301	2	6.5	30	1	CX2A_CONBE	P58625	conus betul
302	2	6.5	30	1	CX7A_CONTU	P58923	conus tulip

303	2	6.5	30	1	CXEX_CONCN	P58928	conus conso
304	2	6.5	30	1	CXK4_CONST	P58921	conus stria
305	2	6.5	30	1	CXVB_CONER	P58783	conus ermin
306	2	6.5	30	1	CY35_DESAC	P81079	desulfuromo
307	2	6.5	30	1	CY01_VIOOD	P82230	viola odora
308	2	6.5	30	1	CY08_VIOOD	P58440	viola odora
309	2	6.5	30	1	DEF2_MACMU	P82317	macaca mula
310	2	6.5	30	1	DIDH_COMTE	P80702	comamonas t
311	2	6.5	30	1	DIU2_HYLLI	P82015	hyles linea
312	2	6.5	30	1	DIU2_MANSE	P24858	manduca sex
313	2	6.5	30	1	END2_ONCKE	P01205	oncorhynchu
314	2	6.5	30	1	FIBR_PANIN	P22775	panulirus i
315	2	6.5	30	1	HCY2_HOMAM	P82297	homarus ame
316	2	6.5	30	1	HETA_RADMA	P58691	radianthus
317	2	6.5	30	1	HYPH_HYBPA	P58445	hybanthus p
318	2	6.5	30	1	IHFB_RHILE	P80606	rhizobium l
319	2	6.5	30	1	ITI1_LAGLE	P26771	lagenaria l
320	2	6.5	30	1	ITR1_CITLA	P11969	citrullus l
321	2	6.5	30	1	ITR1_MOMCH	P10294	momordica c
322	2	6.5	30	1	ITR2_ECBEL	P12071	ecballium e
323	2	6.5	30	1	ITR2_LUFCY	P25850	luffa cylin
324	2	6.5	30	1	ITR3_CUCMC	P32041	cucumis mel
325	2	6.5	30	1	ITR3_MOMCO	P82410	momordica c
326	2	6.5	30	1	ITR4_CUCSA	P10292	cucumis sat
327	2	6.5	30	1	ITR6_CYCPE	P83397	cyclanthera
328	2	6.5	30	1	ITR7_CYCPE	P83398	cyclanthera
329	2	6.5	30	1	KAB5_OLDAF	P58456	oldenlandia
330	2	6.5	30	1	LAS1_PIG	P80171	sus scrofa
331	2	6.5	30	1	LEAH_PHAVU	P81870	phaseolus v
332	2	6.5	30	1	MDH_HELGE	P80037	heliobacter
333	2	6.5	30	1	MMAL_DERMI	P16312	dermatophag
334	2	6.5	30	1	NU5M_PISOC	P24999	pisaster oc
335	2	6.5	30	1	NUO2_SOLTU	P80268	solanum tub
336	2	6.5	30	1	P2CO_ARTSP	P37365	arthrobacte
337	2	6.5	30	1	PCCA_MYXXA	P81185	myxococcus
338	2	6.5	30	1	PCG1_PACGO	P82414	pachycondyl
339	2	6.5	30	1	PCG5_PACGO	P82418	pachycondyl
340	2	6.5	30	1	PETN_NEPOL	Q9tl01	nephroselmi
341	2	6.5	30	1	PLF4_RABIT	P83470	oryctolagus
342	2	6.5	30	1	PLMS_SQUAC	P82542	squalus aca
343	2	6.5	30	1	PMGY_CANAL	P82612	candida alb
344	2	6.5	30	1	PRT1_CLUPA	P02335	clupea pall
345	2	6.5	30	1	PRT2_ONCMY	P02331	oncorhynchu
346	2	6.5	30	1	PRT3_ONCMY	P02332	oncorhynchu
347	2	6.5	30	1	PRT4_ONCMY	P02333	oncorhynchu
348	2	6.5	30	1	PRTB_ONCMY	P12819	oncorhynchu
349	2	6.5	30	1	PSAM_CYACA	Q9tlx5	cyanidium c
350	2	6.5	30	1	PSAM_MESVI	Q9mus2	mesostigma
351	2	6.5	30	1	PSAM_ODOSI	P49487	odontella s
352	2	6.5	30	1	PSAM_PINTH	P41601	pinus thunb
353	2	6.5	30	1	PYSD_METBA	P80524	methanosarc
354	2	6.5	30	1	RIPS_MOMCO	P20655	momordica c
355	2	6.5	30	1	RKGG_LEPKE	P21587	lepidochely
356	2	6.5	30	1	RNP_ODOVI	P19640	odocoileus
357	2	6.5	30	1	SCK2_TITSE	P08816	tityus serr
358	2	6.5	30	1	SCX2_CENLI	P18927	centruroid
359	2	6.5	30	1	SILU_RHIPU	P02885	rhizomucor

360	2	6.5	30	1	TAT_HVIZH	P12512	human immun
361	2	6.5	30	1	TL1X_SPIOL	P82537	spinacia ol
362	2	6.5	30	1	TL29_SPIOL	P81833	spinacia ol
363	2	6.5	30	1	TX2_HETVE	P58426	heteropoda
364	2	6.5	30	1	UC35_MAIZE	P80641	zea mays (m
365	2	6.5	30	1	UDDP_SULAC	P80143	sulfolobus
366	2	6.5	30	1	URE1_ECOLI	Q03284	escherichia
367	2	6.5	30	1	VAA1_EQUAR	Q04236	equisetum a
368	2	6.5	30	1	VAA1_PSINU	Q04237	psilotum nu
369	2	6.5	30	1	VAA2_PSINU	Q04239	psilotum nu
370	2	6.5	30	1	VATN_BOVIN	P81134	bos taurus
371	2	6.5	30	1	VG03_BPPF1	P25137	bacterioph
372	2	6.5	30	1	VPU_HVISC	P05948	human immun
373	2	6.5	30	1	VTTA_BPT3	P20837	bacterioph
374	2	6.5	30	1	Y161_TREPA	O83196	treponema p
375	2	6.5	30	1	Y357_BORBU	O51332	borrelia bu
376	2	6.5	30	1	Y425_BORBU	O51386	borrelia bu
377	2	6.5	30	1	Y573_TREPA	O83583	treponema p
378	2	6.5	30	1	Y932_TREPA	O83902	treponema p
379	2	6.5	30	1	YCCB_ECOLI	P24244	escherichia
380	2	6.5	31	1	A98A_DROME	O46201	drosophila
381	2	6.5	31	1	BCAM_PIG	O19098	sus scrofa
382	2	6.5	31	1	CIRB_CHAPA	P56879	chassalia p
383	2	6.5	31	1	COG5_BOVIN	P83437	bos taurus
384	2	6.5	31	1	COX4_NEUCR	P06809	neurospora
385	2	6.5	31	1	CTRP_PENMO	P35002	penaeus mon
386	2	6.5	31	1	CU54_LOCFI	P11738	locusta mig
387	2	6.5	31	1	CXD6_CONNI	P56710	conus nigro
388	2	6.5	31	1	CXG6_CONTE	P58922	conus texti
389	2	6.5	31	1	CYLA_PSYLO	P56872	psychotria
390	2	6.5	31	1	DEF2_MESAU	P81466	mesocricetu
391	2	6.5	31	1	EFTU_STRLU	P52390	streptomyce
392	2	6.5	31	1	ENDB_CAMDR	P01203	camelus dro
393	2	6.5	31	1	ER29_BOVIN	P81623	bos taurus
394	2	6.5	31	1	ETFD_PARDE	P55932	paracoccus
395	2	6.5	31	1	FIBB_CANFA	P02677	canis famil
396	2	6.5	31	1	GP37_BPSP1	O48393	bacterioph
397	2	6.5	31	1	GT_SERMA	P22416	serratia ma
398	2	6.5	31	1	HBA_MACEU	P81043	macropus eu
399	2	6.5	31	1	HCY1_HOMAM	P82296	homarus ame
400	2	6.5	31	1	HCY2_MAISQ	P82303	maia squina
401	2	6.5	31	1	HEM2_PHAGO	P27687	phascolopsi
402	2	6.5	31	1	LC70_LACPA	P80959	lactobacill
403	2	6.5	31	1	LCCB_LEUME	P81052	leuconostoc
404	2	6.5	31	1	LPRM_ECOLI	P10739	escherichia
405	2	6.5	31	1	MDH_STRAR	P19982	streptomyce
406	2	6.5	31	1	PETL_ANASP	Q8yvq2	anabaena sp
407	2	6.5	31	1	PETL_ARATH	P56776	arabidopsis
408	2	6.5	31	1	PETL_BETVU	P46612	beta vulgar
409	2	6.5	31	1	PETL_CHLVU	P56306	chlorella v
410	2	6.5	31	1	PETL_GUIITH	O78468	guillardia
411	2	6.5	31	1	PETL_MAIZE	P19445	zea mays (m
412	2	6.5	31	1	PETL_ODOSI	P49524	odontella s
413	2	6.5	31	1	PETL_OENHO	Q9mtk4	oenothera h
414	2	6.5	31	1	PETL_ORYSA	P12180	oryza sativ
415	2	6.5	31	1	PETL_PORPU	P51221	porphyra pu
416	2	6.5	31	1	PETL_PSINU	Q8wi03	psilotum nu

417	2	6.5	31	1	PETL_SPIOL	Q9m310	spinacia ol
418	2	6.5	31	1	PETL_WHEAT	P58247	triticum ae
419	2	6.5	31	1	PETM_CYACA	Q9t1r5	cyanidium c
420	2	6.5	31	1	PETN_CYACA	Q9t1r6	cyanidium c
421	2	6.5	31	1	PRT2_CLUPA	P02336	clupea pall
422	2	6.5	31	1	PSAK_ANAVA	P23317	anabaena va
423	2	6.5	31	1	PSAM_CHLVU	P56314	chlorella v
424	2	6.5	31	1	PSAM_CYAPA	P48185	cyanophora
425	2	6.5	31	1	PSBK_SYNVU	P19054	synechococc
426	2	6.5	31	1	PSBM_MESVI	Q9muq7	mesostigma
427	2	6.5	31	1	PSBT_CHLRE	P37256	chlamydomon
428	2	6.5	31	1	PSBT_CHLVU	P56327	chlorella v
429	2	6.5	31	1	PSBT_CYAPA	P48109	cyanophora
430	2	6.5	31	1	PSBT_EUGGR	P20176	euglena gra
431	2	6.5	31	1	PSBT_MESVI	Q9muv6	mesostigma
432	2	6.5	31	1	PSBT_PORPU	P51323	porphyra pu
433	2	6.5	31	1	PYSG_METBA	P80523	methanosarc
434	2	6.5	31	1	RECX_METCL	P37865	methylomona
435	2	6.5	31	1	RL21_STRTR	P48956	streptococc
436	2	6.5	31	1	SARL_HUMAN	O00631	homo sapien
437	2	6.5	31	1	SC37_MESMA	P83407	mesobuthus
438	2	6.5	31	1	SODC_STRHE	P81163	striga herm
439	2	6.5	31	1	TX3_HETVE	P58427	heteropoda
440	2	6.5	31	1	TXA3_PARAC	P09949	parasicyoni
441	2	6.5	31	1	Y191_BORBU	O51209	borrelia bu
442	2	6.5	31	1	Y3KD_BPCHP	P19187	bacterioph
443	2	6.5	31	1	Y603_ARCFU	O29652	archaeoglob
444	2	6.5	32	1	A2M_PACLE	P20738	pacifastacu
445	2	6.5	32	1	APL3_DIAGR	P81471	diatraea gr
446	2	6.5	32	1	ATP0_PIG	P80021	sus scrofa
447	2	6.5	32	1	ATP7_SPIOL	P80088	spinacia ol
448	2	6.5	32	1	ATP0_SPIOL	P80087	spinacia ol
449	2	6.5	32	1	B4G1_RAT	P80225	r beta-1,4-
450	2	6.5	32	1	CAAP_MICEC	P21162	micromonosp
451	2	6.5	32	1	CAL0_BOVIN	P01260	bos taurus
452	2	6.5	32	1	CAL0_PIG	P01259	sus scrofa
453	2	6.5	32	1	CAR1_ECHCA	Q9prp9	echis carin
454	2	6.5	32	1	CEC_OIKKI	P83420	oiketicus k
455	2	6.5	32	1	COA1_BPIF1	O80295	bacterioph
456	2	6.5	32	1	COA1_BPIKE	P03676	bacterioph
457	2	6.5	32	1	COA2_BPFD	P03677	bacterioph
458	2	6.5	32	1	CRP_PLEPL	P12245	pleuronecte
459	2	6.5	32	1	CXG7_CONPE	P56711	conus penna
460	2	6.5	32	1	CYBL_RHOGR	P32953	rhodotorula
461	2	6.5	32	1	CYSB_FASHE	P80529	fasciola he
462	2	6.5	32	1	DBH_SYNY1	P02343	synechocyst
463	2	6.5	32	1	ER29_CHICK	P81628	gallus gall
464	2	6.5	32	1	ER29_TRIVU	P81629	trichosurus
465	2	6.5	32	1	ERH_PIG	P80230	sus scrofa
466	2	6.5	32	1	FER_PORCR	P18821	porphyridiu
467	2	6.5	32	1	FLA1_METHU	P17603	methanospir
468	2	6.5	32	1	FRIH_ANAPL	P80145	anas platyr
469	2	6.5	32	1	GHR4_RAT	P33581	rattus norv
470	2	6.5	32	1	GLB4_LAMSP	P20413	lamellibrac
471	2	6.5	32	1	GT82_DICLA	P82608	dicentrarch
472	2	6.5	32	1	H2AZ_ONCMY	P22647	oncorhynch
473	2	6.5	32	1	HCYC_CHEDE	P83172	cherax dest

474	2	6.5	32	1	IAPP_BOVIN	Q28207	bos taurus
475	2	6.5	32	1	IAPP_SAGOE	Q28934	saguinus oe
476	2	6.5	32	1	IAPP_SHEEP	Q28605	ovis aries
477	2	6.5	32	1	ILVB_ENTAE	Q09129	enterobacte
478	2	6.5	32	1	ITR2_CUCSA	P10291	cucumis sat
479	2	6.5	32	1	LPID_ECOLI	P03060	escherichia
480	2	6.5	32	1	LPID_EDWTA	P08140	edwardsiell
481	2	6.5	32	1	LPIV_ECOLI	P03061	escherichia
482	2	6.5	32	1	MDH_NITAL	P10887	nitzschia a
483	2	6.5	32	1	NEUB_PIG	P01297	sus scrofa
484	2	6.5	32	1	OVOS_ANAPL	P20739	anas platyr
485	2	6.5	32	1	PA22_AGKHP	P18997	agkistrodon
486	2	6.5	32	1	PA2_RHONO	P43318	rhopilema n
487	2	6.5	32	1	PETL_CHLRE	P50369	chlamydomon
488	2	6.5	32	1	PETM_PORPU	P51275	porphyra pu
489	2	6.5	32	1	PHNS_DESMU	P13062	desulfovibr
490	2	6.5	32	1	PRI3_ONCMY	P02330	oncorhynchu
491	2	6.5	32	1	PRT1_ONCKE	P02327	oncorhynchu
492	2	6.5	32	1	PRT4_SCYCA	P30259	scyliorhinu
493	2	6.5	32	1	PRT5_ONCMY	P02334	oncorhynchu
494	2	6.5	32	1	PRT6_ONCMY	P08145	oncorhynchu
495	2	6.5	32	1	PRT7_ONCMY	P08146	oncorhynchu
496	2	6.5	32	1	PRT8_ONCMY	P12817	oncorhynchu
497	2	6.5	32	1	PRT9_ONCMY	P08147	oncorhynchu
498	2	6.5	32	1	PRTA_ONCMY	P12818	oncorhynchu
499	2	6.5	32	1	PRTE_HALME	P28308	halobacteri
500	2	6.5	32	1	PRT_ORYLA	Q91185	oryzias lat
501	2	6.5	32	1	PSBT_CYACA	O19927	cyanidium c
502	2	6.5	32	1	PSBT_GUITH	O78512	guillardia
503	2	6.5	32	1	PSBZ_EUGAN	Q8s195	euglena ana
504	2	6.5	32	1	PSBZ_EUGMY	Q8s191	euglena myx
505	2	6.5	32	1	RIP2_PHYDI	P34967	phytolacca
506	2	6.5	32	1	RK1_RABIT	P81655	oryctolagus
507	2	6.5	32	1	RS19_YEREN	Q56847	yersinia en
508	2	6.5	32	1	SCK2_CENNO	P58504	centruroide
509	2	6.5	32	1	TAT_SIVM2	P05912	simian immu
510	2	6.5	32	1	TRYP_PENMO	P35050	penaeus mon
511	2	6.5	32	1	TX29_PHONI	P29426	phoneutria
512	2	6.5	32	1	TXP7_APTSC	P49271	aptostichus
513	2	6.5	32	1	UC09_MAIZE	P80615	zea mays (m
514	2	6.5	32	1	Y169_TREPA	O83199	treponema p
515	2	6.5	32	1	Y433_BORBU	O51394	borrelia bu
516	2	6.5	32	1	YH17_HAEIN	P44295	haemophilus
517	2	6.5	32	1	YSCA_YEREN	Q01242	yersinia en
518	2	6.5	32	1	YTK3_ILTVT	P23985	infectious
519	2	6.5	33	1	ACT_DICVI	Q24733	dictyocaulu
520	2	6.5	33	1	ALOX_PICPA	P04842	pichia past
521	2	6.5	33	1	ANP3_MYOSC	P04367	myoxocephal
522	2	6.5	33	1	ANP5_MYOAE	P20421	myoxocephal
523	2	6.5	33	1	ATP7_SOLTU	P80496	solanum tub
524	2	6.5	33	1	BR2A_RANES	P40837	rana escule
525	2	6.5	33	1	BR2B_RANES	P40838	rana escule
526	2	6.5	33	1	BR2E_RANES	P32413	rana escule
527	2	6.5	33	1	BR2_RANBP	P32424	rana brevip
528	2	6.5	33	1	CECB_HELVI	P83414	heliiothis v
529	2	6.5	33	1	CECC_HELVI	P83415	heliiothis v
530	2	6.5	33	1	COA1_BPFD	P03675	bacterioph

531	2	6.5	33	1	COA2_BPI22	P15414	bacterioph
532	2	6.5	33	1	COA2_BPIKE	P03678	bacterioph
533	2	6.5	33	1	COXL_ONCMY	P80330	oncorhynch
534	2	6.5	33	1	CU89_HUMAN	P59042	homo sapien
535	2	6.5	33	1	CXBW_CONRA	P58804	conus radia
536	2	6.5	33	1	CXO_CONVE	P83301	conus ventr
537	2	6.5	33	1	DBB2_DOLAU	P83376	dolabella a
538	2	6.5	33	1	DEF1_MESAU	P81465	mesocricetu
539	2	6.5	33	1	DEF3_MESAU	P81467	mesocricetu
540	2	6.5	33	1	DEF4_MESAU	P81468	mesocricetu
541	2	6.5	33	1	DHE3_PIG	P42174	sus scrofa
542	2	6.5	33	1	FER_PORAE	P18820	porphyridiu
543	2	6.5	33	1	GAST_CAVPO	P06885	cavia porce
544	2	6.5	33	1	GAST_CHIBR	P10034	chinchilla
545	2	6.5	33	1	GAST_DIDMA	P33713	didelphis m
546	2	6.5	33	1	GGN2_RANRU	P80396	rana rugosa
547	2	6.5	33	1	GGN3_RANRU	P80397	rana rugosa
548	2	6.5	33	1	HF40_MAIZE	P82865	zea mays (m
549	2	6.5	33	1	HOXU_RHOOP	P22659	rhodococcus
550	2	6.5	33	1	LPPY_SALTY	P08522	salmonella
551	2	6.5	33	1	LPRH_ECOLI	P37324	escherichia
552	2	6.5	33	1	LYC2_HORSE	P81710	equus cabal
553	2	6.5	33	1	MBP1_MAIZE	P28794	zea mays (m
554	2	6.5	33	1	MHAA_STRCH	P80435	streptomyce
555	2	6.5	33	1	MYMY_MYTED	P81614	mytilus edu
556	2	6.5	33	1	OTCC_PSEPU	P11727	pseudomonas
557	2	6.5	33	1	PEN3_ADECU	P35987	canine aden
558	2	6.5	33	1	PETM_CYAPA	P48366	cyanophora
559	2	6.5	33	1	PETM_SYNEL	Q8dj15	synechococc
560	2	6.5	33	1	PK1_DICDI	P34101	dictyosteli
561	2	6.5	33	1	PK5_DICDI	P34104	dictyosteli
562	2	6.5	33	1	PRI1_ONCMY	P02326	oncorhynch
563	2	6.5	33	1	PRI2_ONCMY	P02328	oncorhynch
564	2	6.5	33	1	PRTB_MUGCE	P08130	mugil cepha
565	2	6.5	33	1	PRTL_ECOLI	P02338	escherichia
566	2	6.5	33	1	PSAK_CUCSA	P42051	cucumis sat
567	2	6.5	33	1	PSBT_ARATH	P37259	arabidopsis
568	2	6.5	33	1	PSBT_MAIZE	P37257	zea mays (m
569	2	6.5	33	1	RL21_XENLA	P49628	xenopus lae
570	2	6.5	33	1	RL26_XENLA	P49629	xenopus lae
571	2	6.5	33	1	RL28_XENLA	P46780	xenopus lae
572	2	6.5	33	1	RL4_HALCU	P05967	halobacteri
573	2	6.5	33	1	RPOC_HETCA	P36441	heterosigma
574	2	6.5	33	1	RRPO_BPBZ1	P09674	bacterioph
575	2	6.5	33	1	RS4_XENLA	P49401	xenopus lae
576	2	6.5	33	1	RT25_BOVIN	P82669	bos taurus
577	2	6.5	33	1	RUGA_RANRU	P80954	rana rugosa
578	2	6.5	33	1	SCX9_BUTO	P04099	buthus occi
579	2	6.5	33	1	THIO_CLOST	P81109	clostridium
580	2	6.5	33	1	TX1_HETVE	P58425	heteropoda
581	2	6.5	33	1	TXH1_SELHU	P56676	selenocosmi
582	2	6.5	33	1	TXN3_SELHA	P83464	selenocosmi
583	2	6.5	33	1	VT1B_RAT	P58200	rattus norv
584	2	6.5	33	1	Y474_BORBU	O51430	borrelia bu
585	2	6.5	33	1	Y656_TREPA	O83662	treponema p
586	2	6.5	33	1	Y849_BORBU	O51789	borrelia bu
587	2	6.5	33	1	YC12_CHLRE	P50370	chlamydomon

588	2	6.5	33	1	YC12_MARPO	P31560	marchantia
589	2	6.5	33	1	YC12_MESVI	Q9mus3	mesostigma
590	2	6.5	33	1	YC12_NEPOL	Q9tky6	nephroselmi
591	2	6.5	33	1	YC12_PINTH	P41600	pinus thunb
592	2	6.5	33	1	YL74_ARCFU	O28108	archaeoglob
593	2	6.5	33	1	YLCH_BP82	Q37869	bacterioph
594	2	6.5	33	1	YLCH_ECOLI	Q47268	escherichia
595	2	6.5	34	1	AMP2_CHICK	P80390	gallus gall
596	2	6.5	34	1	ASPG_PIG	P30918	sus scrofa
597	2	6.5	34	1	BR2C_RANES	P40839	rana escule
598	2	6.5	34	1	COL_CHICK	P11148	gallus gall
599	2	6.5	34	1	COXA_THETH	P82543	thermus the
600	2	6.5	34	1	COXG_THUOB	P80976	thunnus obe
601	2	6.5	34	1	CXGS_CONGE	P15472	conus geogr
602	2	6.5	34	1	DEF2_RABIT	P07468	oryctolagus
603	2	6.5	34	1	DEF7_RABIT	P80223	oryctolagus
604	2	6.5	34	1	ECAB_ECTTU	P49344	ectatomma t
605	2	6.5	34	1	EF2_RABIT	P55823	oryctolagus
606	2	6.5	34	1	EGGR_APLCA	P01363	aplysia cal
607	2	6.5	34	1	H1S_STRPU	P19376	strongyloce
608	2	6.5	34	1	HS7S_CUCMA	P31082	cucurbita m
609	2	6.5	34	1	ITR1_MOMCO	P82408	momordica c
610	2	6.5	34	1	ITR2_MOMCO	P82409	momordica c
611	2	6.5	34	1	LPTN_PROVU	P28779	proteus vul
612	2	6.5	34	1	M44E_HUMAN	Q96pg1	homo sapien
613	2	6.5	34	1	MYTB_MYTED	P81613	mytilus edu
614	2	6.5	34	1	PETM_ANASP	Q9f4w2	anabaena sp
615	2	6.5	34	1	PRT1_SAROR	P25327	sarda orien
616	2	6.5	34	1	PRT1_SCOSC	P83264	scomber sco
617	2	6.5	34	1	PRT1_THUTH	P02321	thunnus thy
618	2	6.5	34	1	PRT2_SCOSC	P83265	scomber sco
619	2	6.5	34	1	PRT2_THUTH	P02322	thunnus thy
620	2	6.5	34	1	PRT_DICLA	Q9ps27	dicentrarch
621	2	6.5	34	1	PRT_PERFV	P29629	perca flave
622	2	6.5	34	1	PSAI_LOTJA	Q9bbs0	lotus japon
623	2	6.5	34	1	PSAI_OENHO	Q9mtl2	oenothera h
624	2	6.5	34	1	PSBM_ARATH	P12169	arabidopsis
625	2	6.5	34	1	PSBM_CHAGL	Q8ma15	chaetosphae
626	2	6.5	34	1	PSBM_CHLRE	P92277	chlamydomon
627	2	6.5	34	1	PSBM_MAIZE	P48189	zea mays (m
628	2	6.5	34	1	PSBM_MARPO	P12168	marchantia
629	2	6.5	34	1	PSBM_NEPOL	Q9tl37	nephroselmi
630	2	6.5	34	1	PSBM_OENHO	Q9mtm8	oenothera h
631	2	6.5	34	1	PSBM_PEA	P34833	pisum sativ
632	2	6.5	34	1	PSBM_PSINU	Q8wi22	psilotum nu
633	2	6.5	34	1	PSBM_WHEAT	Q9xps6	triticum ae
634	2	6.5	34	1	PSBT_TOBAC	P12184	nicotiana t
635	2	6.5	34	1	PSPC_BOVIN	P15783	bos taurus
636	2	6.5	34	1	PSPC_CANFA	P22397	canis famil
637	2	6.5	34	1	PYSB_METBA	P80522	methanosarc
638	2	6.5	34	1	RNLI_PIG	P15466	sus scrofa
639	2	6.5	34	1	RR2_OCHNE	Q40606	ochrosphaer
640	2	6.5	34	1	SCXM_SCOMA	P80719	scorpio mau
641	2	6.5	34	1	SMS_MYXGL	P19209	myxine glut
642	2	6.5	34	1	THEM_MALSU	P13858	malbranchea
643	2	6.5	34	1	TX33_PHONI	P81789	phoneutria
644	2	6.5	34	1	TXP5_BRASM	P49266	brachypelma

645	2	6.5	34	1	VLYS_BPM1	P08229	bacterioph
646	2	6.5	34	1	VPU_HV1W2	P08808	human immun
647	2	6.5	34	1	Y05J_BPT4	P39239	bacterioph
648	2	6.5	34	1	Y224_TREPA	O83253	treponema p
649	2	6.5	34	1	Y848_BORBU	O51788	borrelia bu
650	2	6.5	34	1	Y870_HAEIN	P44065	haemophilus
651	2	6.5	34	1	Y967_HAEIN	P44086	haemophilus
652	2	6.5	34	1	YC12_GUITH	O78460	guillardia
653	2	6.5	34	1	YC12_ODOSI	P49529	odontella s
654	2	6.5	34	1	YC12_PORPU	P51385	porphyra pu
655	2	6.5	34	1	YC12_SKECO	O96797	skeletonema
656	2	6.5	34	1	YMIA_AGR TU	P38437	agrobacteri
657	2	6.5	34	1	Z33B_HUMAN	Q06731	homo sapien
658	2	6.5	35	1	ADO1_AGRDO	P58608	agriosphodr
659	2	6.5	35	1	C550_BACHA	P80091	bacillus ha
660	2	6.5	35	1	CEC4_BOMMO	P14666	bombyx mori
661	2	6.5	35	1	CECA_HELVI	P83413	heliiothis v
662	2	6.5	35	1	CECB_ANTPE	P01509	antheraea p
663	2	6.5	35	1	CHI1_CASSA	P29137	castanea sa
664	2	6.5	35	1	D3HI_RABIT	P32185	oryctolagus
665	2	6.5	35	1	DEFB_MYTED	P81611	mytilus edu
666	2	6.5	35	1	END4_YEREN	P42691	yersinia en
667	2	6.5	35	1	ERFK_KLEAE	Q08599	klebsiella
668	2	6.5	35	1	EXE2_HEL SU	P04204	heloderma s
669	2	6.5	35	1	FAS_CAPHI	P08757	capra hircu
670	2	6.5	35	1	FLAV_NOSSM	P35707	nostoc sp.
671	2	6.5	35	1	GBGU_MOUSE	Q61017	mus muscul
672	2	6.5	35	1	GRDB_CLOPU	P55793	clostridium
673	2	6.5	35	1	GUR_GYMSY	P25810	gymnema syl
674	2	6.5	35	1	HCYA_CHEDE	P83173	cherax dest
675	2	6.5	35	1	HMWC_DESGI	P38588	desulfovibr
676	2	6.5	35	1	IAAC_HORVU	P34951	hordeum vul
677	2	6.5	35	1	KPPR_PINPS	P81664	pinus pinas
678	2	6.5	35	1	LCGB_LACLA	P36962	lactococcus
679	2	6.5	35	1	NEF_HV1H3	P05854	human immun
680	2	6.5	35	1	PBP1_LYMDI	P34176	lymantria d
681	2	6.5	35	1	PBP2_LYMDI	P34177	lymantria d
682	2	6.5	35	1	PBP_HYACE	P34175	hyalophora
683	2	6.5	35	1	PHI1_MYTCA	P35422	mytilus cal
684	2	6.5	35	1	PSAI_CYAPA	P48116	cyanophora
685	2	6.5	35	1	PSBT_MARPO	P12182	marchantia
686	2	6.5	35	1	PSBT_OENHO	P37258	oenothera h
687	2	6.5	35	1	PSBT_ORYSA	P12183	oryza sativ
688	2	6.5	35	1	PSBT_PINTH	P41625	pinus thunb
689	2	6.5	35	1	PSPC_PIG	P15785	sus scrofa
690	2	6.5	35	1	RL32_HALCU	P05965	halobacteri
691	2	6.5	35	1	SCKB_PANIM	P55928	pandinus im
692	2	6.5	35	1	SCKG_PANIM	Q10726	pandinus im
693	2	6.5	35	1	SCX1_BUTSI	P15229	buthus sind
694	2	6.5	35	1	SCX5_BUTEU	P15222	buthus eupe
695	2	6.5	35	1	SCXP_ANDMA	P01498	androctonus
696	2	6.5	35	1	SMS_LAMFL	Q9prro	lampetra fl
697	2	6.5	35	1	SPRC_PIG	P20112	sus scrofa
698	2	6.5	35	1	THPA_THADA	P21381	thaumatococ
699	2	6.5	35	1	TMTX_MESTA	Q9bn12	mesobuthus
700	2	6.5	35	1	TXAG_AGEOP	P31328	agelena opu
701	2	6.5	35	1	TXH4_SELHU	P83303	selenocosmi

702	2	6.5	35	1	TXKS_STOHE	P29187	stoichactis
703	2	6.5	35	1	TXN4_SELHA	P83471	selenocosmi
704	2	6.5	35	1	VL3_PAPVD	P06919	deer papill
705	2	6.5	35	1	VSPA_CERVI	P18692	cerastes vi
706	2	6.5	35	1	WSP7_PINPS	P81086	pinus pinas
707	2	6.5	35	1	Y210_HAEIN	P43964	haemophilus
708	2	6.5	35	1	Y320_BORBU	O51299	borrelia bu
709	2	6.5	35	1	Y37_BPT3	P20325	bacterioph
710	2	6.5	35	1	Y644_ARCFU	O29613	archaeoglob
711	2	6.5	35	1	Y845_BORBU	O51785	borrelia bu
712	2	6.5	35	1	Y847_BORBU	O51787	borrelia bu
713	2	6.5	35	1	YC12_CYACA	Q9tlx0	cyanidium c
714	2	6.5	35	1	YC69_ARCFU	O28999	archaeoglob
715	2	6.5	35	1	YQB5_CAEEL	Q09258	caenorhabdi
716	2	6.5	36	1	AMPL_PIG	P28839	sus scrofa
717	2	6.5	36	1	ANFV_ANGJA	P22642	anguilla ja
718	2	6.5	36	1	C3L1_BOVIN	P30922	bos taurus
719	2	6.5	36	1	CBBA_NITVU	P37102	nitrobacter
720	2	6.5	36	1	CECD_ANTPE	P01511	antheraea p
721	2	6.5	36	1	CYC7_GEOME	P81894	geobacter m
722	2	6.5	36	1	DESR_DESGI	P00273	desulfovibr
723	2	6.5	36	1	F4RE_METOG	P80951	methanogeni
724	2	6.5	36	1	GLU1_ORENI	P81026	oreochromis
725	2	6.5	36	1	GLUC_HYDCO	P09682	hydrolagus
726	2	6.5	36	1	H1L5_ENSMI	P27203	ensis minor
727	2	6.5	36	1	HBB_PONPY	Q9tt34	pongo pygma
728	2	6.5	36	1	IAA_STRAU	P04082	streptomyce
729	2	6.5	36	1	IOB1_ISYOB	P58609	isyndus obs
730	2	6.5	36	1	KAD_STRGR	P53398	streptomyce
731	2	6.5	36	1	LHG_RHOVI	P04126	rhodopseudo
732	2	6.5	36	1	LYOX_PIG	P45845	sus scrofa
733	2	6.5	36	1	MFA1_YEAST	P34165	saccharomyc
734	2	6.5	36	1	MPG2_DACGL	Q41183	dactylis gl
735	2	6.5	36	1	MYPC_RAT	P56741	rattus norv
736	2	6.5	36	1	NEUH_CARCA	P11975	cardisoma c
737	2	6.5	36	1	NEUY_GADMO	P80167	gadus morhu
738	2	6.5	36	1	NEUY_ONCMY	P29071	oncorhynch
739	2	6.5	36	1	NEUY_RABIT	P09640	oryctolagus
740	2	6.5	36	1	NEUY_RANRI	P29949	rana ridibu
741	2	6.5	36	1	NIFH_ENTAG	P26249	enterobacte
742	2	6.5	36	1	NLTP_PINPI	P26912	pinus pinea
743	2	6.5	36	1	NUCM_SOLTU	P80264	solanum tub
744	2	6.5	36	1	OST2_CHICK	P80897	gallus gall
745	2	6.5	36	1	PAHO_ALLMI	P06305	alligator m
746	2	6.5	36	1	PAHO_ANSAN	P06304	anser anser
747	2	6.5	36	1	PAHO_CERSI	P37999	ceratotheri
748	2	6.5	36	1	PAHO_DIDMA	P18107	didelphis m
749	2	6.5	36	1	PAHO_EQUZE	P38000	equus zebra
750	2	6.5	36	1	PAHO_ERIEU	P41335	erinaceus e
751	2	6.5	36	1	PAHO_LARAR	P41337	larus argen
752	2	6.5	36	1	PAHO_MACMU	P33684	macaca mula
753	2	6.5	36	1	PAHO_RABIT	P41336	oryctolagus
754	2	6.5	36	1	PAHO_RANCA	P15427	rana catesb
755	2	6.5	36	1	PAHO_RANTE	P31229	rana tempor
756	2	6.5	36	1	PAHO_STRCA	P11967	struthio ca
757	2	6.5	36	1	PAHO_TAPPI	P39659	tapirus pin
758	2	6.5	36	1	PGKH_CHLFU	P36232	chlorella f

759	2	6.5	36	1	PMY_PETMA	P80024	petromyzon
760	2	6.5	36	1	PSAD_PEA	P20117	pisum sativ
761	2	6.5	36	1	PSAH_PEA	P20121	pisum sativ
762	2	6.5	36	1	PSAI_ANGLY	P28251	angiopteris
763	2	6.5	36	1	PSAI_BRAOL	Q31909	brassica ol
764	2	6.5	36	1	PSAI_CHAGL	Q8m9x5	chaetosphae
765	2	6.5	36	1	PSAI_CHLVU	P58214	chlorella v
766	2	6.5	36	1	PSAI_CYACA	Q9tm24	cyanidium c
767	2	6.5	36	1	PSAI_GUITH	O78462	guillardia
768	2	6.5	36	1	PSAI_HORVU	P13165	hordeum vul
769	2	6.5	36	1	PSAI_MAIZE	P30980	zea mays (m
770	2	6.5	36	1	PSAI_MARPO	P12185	marchantia
771	2	6.5	36	1	PSAI_MESVI	Q9muq4	mesostigma
772	2	6.5	36	1	PSAI_NEPOL	Q9tl12	nephroselmi
773	2	6.5	36	1	PSAI_ORYSA	P12186	oryza sativ
774	2	6.5	36	1	PSAI_PICAB	O47040	picea abies
775	2	6.5	36	1	PSAI_PORPU	P51387	porphyra pu
776	2	6.5	36	1	PSAI_PSINU	Q8wi10	psilotum nu
777	2	6.5	36	1	PSAI_SKECO	O96813	skeletonema
778	2	6.5	36	1	PSAI_TOBAC	P12187	nicotiana t
779	2	6.5	36	1	PSAI_WHEAT	P25410	triticum ae
780	2	6.5	36	1	PSBI_ARATH	P09970	arabidopsis
781	2	6.5	36	1	PSBI_HORVU	P25876	hordeum vul
782	2	6.5	36	1	PSBI_MARPO	P09969	marchantia
783	2	6.5	36	1	PSBI_ORYSA	P12161	oryza sativ
784	2	6.5	36	1	PSBI_PINTH	P41599	pinus thunb
785	2	6.5	36	1	PSBI_PSEMZ	P29796	pseudotsuga
786	2	6.5	36	1	PSBM_CHLVU	P56325	chlorella v
787	2	6.5	36	1	PSBM_SYNEL	Q8dha7	synechococc
788	2	6.5	36	1	PSBY_ODOSI	P49543	odontella s
789	2	6.5	36	1	PSBY_PORPU	P51206	porphyra pu
790	2	6.5	36	1	PYY_AMICA	P29205	amia calva
791	2	6.5	36	1	PYY_LEPSP	P09473	lepisosteus
792	2	6.5	36	1	PYY_MYOSC	P09641	myoxocephal
793	2	6.5	36	1	PYY_ONCKI	P09474	oncorhynchu
794	2	6.5	36	1	PYY_ORENI	P81028	oreochromis
795	2	6.5	36	1	PYY_PIG	P01305	sus scrofa
796	2	6.5	36	1	PYY_RAJRH	P29206	raja rhina
797	2	6.5	36	1	PYY_RANRI	P29204	rana ridibu
798	2	6.5	36	1	SCK2_CENLL	P45630	centruroide
799	2	6.5	36	1	SCK3_LEIQH	P45660	leiurus qui
800	2	6.5	36	1	SCX1_BUTEU	P15220	buthus eupe
801	2	6.5	36	1	SCXL_LEIQU	P45639	leiurus qui
802	2	6.5	36	1	SPYY_PHYBI	P80952	phyllomedus
803	2	6.5	36	1	TAEK_ACTEQ	P81897	actinia equ
804	2	6.5	36	1	TLN1_CHICK	P54939	gallus gall
805	2	6.5	36	1	TX1B_AGEAP	P15970	agelenopsis
806	2	6.5	36	1	TX35_PHONI	P81791	phoneutria
807	2	6.5	36	1	TXAM_METSE	P11495	metridium s
808	2	6.5	36	1	TXD3_PARLU	P83258	paracoelote
809	2	6.5	36	1	TXJB_HADVE	P82226	hadronyche
810	2	6.5	36	1	Y16L_BPT4	P39244	bacterioph
811	2	6.5	36	1	Y297_ARCFU	O29945	archaeoglob
812	2	6.5	36	1	Y4KD_BPCHP	P19188	bacterioph
813	2	6.5	36	1	Y609_BORBU	O51554	borrelia bu
814	2	6.5	36	1	Y619_ARCFU	O29636	archaeoglob
815	2	6.5	36	1	Y699_TREPA	O83697	treponema p

816	2	6.5	36	1	YC12_CYAPA	P48256	cyanophora
817	2	6.5	36	1	YG50_HAEIN	P44281	haemophilus
818	2	6.5	36	1	YRKG_BACSU	P54434	bacillus su
819	2	6.5	37	1	24KD_PLACH	P14592	plasmodium
820	2	6.5	37	1	AFP4_MALPA	P83138	malva parvi
821	2	6.5	37	1	ANP3_PSEAM	P02733	pseudopleur
822	2	6.5	37	1	ATPO_SOLTU	P80504	solanum tub
823	2	6.5	37	1	B2MG_ORENI	Q03423	oreochromis
824	2	6.5	37	1	CAL1_PIG	P30880	sus scrofa
825	2	6.5	37	1	CEC2_MANSE	P14662	manduca sex
826	2	6.5	37	1	CEC3_MANSE	P14663	manduca sex
827	2	6.5	37	1	CEC4_MANSE	P14664	manduca sex
828	2	6.5	37	1	CG2S_LUPAN	P09930	lupinus ang
829	2	6.5	37	1	CHCD_ANTPO	P08931	antheraea p
830	2	6.5	37	1	CS40_STAAU	P81684	staphylococ
831	2	6.5	37	1	CUP4_SARBU	P14486	sarcophaga
832	2	6.5	37	1	DEFA_MYTED	P81610	mytilus edu
833	2	6.5	37	1	ECAA_ECTTU	P49343	ectatomma t
834	2	6.5	37	1	ES2A_RANES	P40845	rana escule
835	2	6.5	37	1	ES2B_RANES	P40846	rana escule
836	2	6.5	37	1	F13A_BOVIN	P12260	bos taurus
837	2	6.5	37	1	GHR3_RAT	P33580	rattus norv
838	2	6.5	37	1	HCYB_CANPG	P83175	cancer pagu
839	2	6.5	37	1	HOXF_RHOOP	P22658	rhodococcus
840	2	6.5	37	1	LPPY_SERMA	P19937	serratia ma
841	2	6.5	37	1	MAUR_PARVE	Q56462	paracoccus
842	2	6.5	37	1	ME20_EUPRA	P26888	euplotes ra
843	2	6.5	37	1	ME22_EUPRA	P58548	euplotes ra
844	2	6.5	37	1	MIBP_PSESP	P04576	pseudomonas
845	2	6.5	37	1	NLT3_VITSX	P80273	vitis sp. (
846	2	6.5	37	1	NLT4_VITSX	P80274	vitis sp. (
847	2	6.5	37	1	NUFM_SOLTU	P80266	solanum tub
848	2	6.5	37	1	OP2A_OXYKI	P83248	oxyopes kit
849	2	6.5	37	1	OP2B_OXYKI	P83249	oxyopes kit
850	2	6.5	37	1	OP2C_OXYKI	P83250	oxyopes kit
851	2	6.5	37	1	OP2D_OXYKI	P83251	oxyopes kit
852	2	6.5	37	1	PETG_ANASP	P58246	anabaena sp
853	2	6.5	37	1	PETG_ANAVA	Q913p7	anabaena va
854	2	6.5	37	1	PETG_ARATH	P56775	arabidopsis
855	2	6.5	37	1	PETG_CHAGL	Q8m9y4	chaetosphae
856	2	6.5	37	1	PETG_CHLEU	P46304	chlamydomon
857	2	6.5	37	1	PETG_CHLRE	Q08362	chlamydomon
858	2	6.5	37	1	PETG_CHLVU	P56305	chlorella v
859	2	6.5	37	1	PETG_CUSRE	P30398	cuscuta ref
860	2	6.5	37	1	PETG_CYAPA	P14236	cyanophora
861	2	6.5	37	1	PETG_EUGGR	P30396	euglena gra
862	2	6.5	37	1	PETG_GUI TH	O78505	guillardia
863	2	6.5	37	1	PETG_MARPO	P12120	marchantia
864	2	6.5	37	1	PETG_MESVI	Q9mun3	mesostigma
865	2	6.5	37	1	PETG_NEPOL	Q9tky8	nephroselmi
866	2	6.5	37	1	PETG_ODOSI	P49470	odontella s
867	2	6.5	37	1	PETG_ORYSA	P12121	oryza sativ
868	2	6.5	37	1	PETG_PINTH	P41614	pinus thunb
869	2	6.5	37	1	PETG_PORPU	P51318	porphyra pu
870	2	6.5	37	1	PETG_PSINU	Q8wi02	psilotum nu
871	2	6.5	37	1	PETG_SKECO	O96811	skeletonema
872	2	6.5	37	1	PETG_SYNEL	Q8dki2	synechococc

873	2	6.5	37	1	PETG_SYNPF	Q9z3g1	synechococc
874	2	6.5	37	1	PIIL_ACHLY	P81720	achromobact
875	2	6.5	37	1	POLN_WEEV	P13896	western equ
876	2	6.5	37	1	PRF1_RAT	P18889	rattus norv
877	2	6.5	37	1	PSAI_ARATH	P56768	arabidopsis
878	2	6.5	37	1	PSAJ_EUGGR	P30394	euglena gra
879	2	6.5	37	1	PSBL_ARATH	P29301	arabidopsis
880	2	6.5	37	1	PSBL_ORYSA	P12166	oryza sativ
881	2	6.5	37	1	PSBM_PINTH	P41608	pinus thunb
882	2	6.5	37	1	PSBY_CYACA	O19893	cyanidium c
883	2	6.5	37	1	PSBY_GUITH	O78433	guillardia
884	2	6.5	37	1	PYY_CHICK	P29203	gallus gall
885	2	6.5	37	1	REV_SIVM2	P08809	simian immu
886	2	6.5	37	1	RK36_ARATH	P12144	arabidopsis
887	2	6.5	37	1	RK36_ASTLO	P24355	astasia lon
888	2	6.5	37	1	RK36_CHAGL	Q8m9v5	chaetosphae
889	2	6.5	37	1	RK36_CHLVU	P56360	chlorella v
890	2	6.5	37	1	RK36_CYACA	Q9tlu9	cyanidium c
891	2	6.5	37	1	RK36_CYAPA	P48131	cyanophora
892	2	6.5	37	1	RK36_EPIVI	P30069	epifagus vi
893	2	6.5	37	1	RK36_EUGGR	P21532	euglena gra
894	2	6.5	37	1	RK36_LOTJA	Q9bbq2	lotus japon
895	2	6.5	37	1	RK36_MARPO	P12142	marchantia
896	2	6.5	37	1	RK36_NEPOL	Q9tl26	nephroselmi
897	2	6.5	37	1	RK36_ODOSI	P49568	odontella s
898	2	6.5	37	1	RK36_OENHO	Q9mtj1	oenothera h
899	2	6.5	37	1	RK36_ORYSA	P12143	oryza sativ
900	2	6.5	37	1	RK36_PEA	P07815	pisum sativ
901	2	6.5	37	1	RK36_PINTH	P41631	pinus thunb
902	2	6.5	37	1	RK36_PORPU	P51296	porphyra pu
903	2	6.5	37	1	RK36_PSINU	Q8why9	psilotum nu
904	2	6.5	37	1	RK36_SPIOL	P12230	spinacia ol
905	2	6.5	37	1	RL36_ANASP	Q8ypk0	anabaena sp
906	2	6.5	37	1	RL36_AQUAE	O66487	aquifex aeo
907	2	6.5	37	1	RL36_BACHD	O50631	bacillus ha
908	2	6.5	37	1	RL36_BACST	P07841	bacillus st
909	2	6.5	37	1	RL36_BACSU	P20278	bacillus su
910	2	6.5	37	1	RL36_BORBU	O51452	borrelia bu
911	2	6.5	37	1	RL36_CAMJE	Q9pm84	campylobact
912	2	6.5	37	1	RL36_CLOAB	Q97ek2	clostridium
913	2	6.5	37	1	RL36_CLOPE	Q8xhu7	clostridium
914	2	6.5	37	1	RL36_DEIRA	Q9rsk0	deinococcus
915	2	6.5	37	1	RL36_HAEIN	P46361	haemophilus
916	2	6.5	37	1	RL36_HELPJ	Q9zjt1	helicobacte
917	2	6.5	37	1	RL36_HELPY	P56058	helicobacte
918	2	6.5	37	1	RL36_LEPIN	Q9xd13	leptospira
919	2	6.5	37	1	RL36_LISMO	Q927n0	listeria mo
920	2	6.5	37	1	RL36_MYCGA	Q9rdv9	mycoplasma
921	2	6.5	37	1	RL36_MYCGE	P47420	mycoplasma
922	2	6.5	37	1	RL36_MYCLE	Q9x7a2	mycobacteri
923	2	6.5	37	1	RL36_MYCPN	P52864	mycoplasma
924	2	6.5	37	1	RL36_MYCPU	Q98q05	mycoplasma
925	2	6.5	37	1	RL36_MYCSP	P38015	mycoplasma
926	2	6.5	37	1	RL36_MYCTU	P45810	mycobacteri
927	2	6.5	37	1	RL36_NEIMA	Q9jrb2	neisseria m
928	2	6.5	37	1	RL36_STAAM	Q99s42	staphylococ
929	2	6.5	37	1	RL36_STRCO	O86772	streptomyce

930	2	6.5	37	1	RL36_SYNPE	024707	synechococc
931	2	6.5	37	1	RL36_THETH	P80256	thermus the
932	2	6.5	37	1	RL36_THETN	Q8r7x8	thermoanaer
933	2	6.5	37	1	RL36_TREPA	O83239	treponema p
934	2	6.5	37	1	RL36_UREPA	Q9pqn7	ureaplasma
935	2	6.5	37	1	RL36_VIBCH	P78001	vibrio chol
936	2	6.5	37	1	RL7_CLOPA	P05393	clostridium
937	2	6.5	37	1	RS15_HELLU	P52820	helix lucor
938	2	6.5	37	1	RUGC_RANRU	P80956	rana rugosa
939	2	6.5	37	1	SCIT_MESTA	P81761	mesobuthus
940	2	6.5	37	1	SCK2_LEIQH	P45628	leiurus qui
941	2	6.5	37	1	SCK3_BUTOC	P59290	buthus occi
942	2	6.5	37	1	SCK3_PARTR	P83112	parabuthus
943	2	6.5	37	1	SCKA_TITSE	P46114	tityus serr
944	2	6.5	37	1	SCKC_LEIQH	P13487	leiurus qui
945	2	6.5	37	1	SMS_PETMA	P21779	petromyzon
946	2	6.5	37	1	TCTP_TRYBB	P35758	trypanosoma
947	2	6.5	37	1	THHS_HORVU	P33045	hordeum vul
948	2	6.5	37	1	TX21_SELHU	P82959	selenocosmi
949	2	6.5	37	1	TX22_SELHU	P82960	selenocosmi
950	2	6.5	37	1	TXD1_PARLU	P83256	paracoelote
951	2	6.5	37	1	TXD2_PARLU	P83257	paracoelote
952	2	6.5	37	1	TXD4_PARLU	P83259	paracoelote
953	2	6.5	37	1	TXJC_HADVE	P82228	hadronyche
954	2	6.5	37	1	TXKB_BUNGR	P29186	bunodosoma
955	2	6.5	37	1	TXOF_HADVE	P81599	hadronyche
956	2	6.5	37	1	TXP3_APTSC	P49268	aptostichus
957	2	6.5	37	1	VA1_BBBF2	P19347	bacterioph
958	2	6.5	37	1	VG40_BPML5	Q05250	mycobacteri
959	2	6.5	37	1	VG65_BPPH2	P16515	bacterioph
960	2	6.5	37	1	VG65_BPPZA	P08384	bacterioph
961	2	6.5	37	1	VGJ_BPPHX	P03651	bacterioph
962	2	6.5	37	1	VP64_NPVBM	P41722	bombyx mori
963	2	6.5	37	1	VPU_HV1Z8	P08807	human immun
964	2	6.5	37	1	Y268_ARCFU	O29971	archaeoglob
965	2	6.5	37	1	Y63_BPT7	P03799	bacterioph
966	2	6.5	37	1	Y692_BORBU	O51635	borrelia bu
967	2	6.5	37	1	Y700_BORBU	O51643	borrelia bu
968	2	6.5	37	1	Y762_BORBU	O51703	borrelia bu
969	2	6.5	37	1	Y846_BORBU	O51786	borrelia bu
970	2	6.5	37	1	YBGT_ECOLI	P56100	escherichia
971	2	6.5	37	1	YC12_CHLVU	P56328	chlorella v
972	2	6.5	37	1	YDA3_SCHPO	Q10345	schizosacch
973	2	6.5	37	1	YIM4_BPPH1	P10428	bacterioph
974	2	6.5	37	1	YQGE_BACCA	P28753	bacillus ca
975	2	6.5	37	1	YRYL_CAEEL	Q19177	caenorhabdi
976	2	6.5	38	1	AFP5_MALPA	P83139	malva parvi
977	2	6.5	38	1	BD01_BOVIN	P46159	bos taurus
978	2	6.5	38	1	BD08_BOVIN	P46166	bos taurus
979	2	6.5	38	1	COA3_XANCP	Q07484	xanthomonas
980	2	6.5	38	1	CRS3_NOTGO	P15534	nototodarus
981	2	6.5	38	1	CU47_LACCU	P80323	lactobacill
982	2	6.5	38	1	DCHS_MICSP	P00863	micrococcus
983	2	6.5	38	1	DEF4_LEIQH	P41965	leiurus qui
984	2	6.5	38	1	DEF7_SPIOL	P81573	spinacia ol
985	2	6.5	38	1	DEFI_AESCY	P80154	aeschna cya
986	2	6.5	38	1	DEFI_MYTGA	P80571	mytilus gal

987	2	6.5	38	1	DLP3_ORNAN	P82141	ornithorhyn
988	2	6.5	38	1	DPOB_BOVIN	Q27958	bos taurus
989	2	6.5	38	1	E2F1_RAT	O09139	rattus norv
990	2	6.5	38	1	EST5_DROMO	P10095	drosophila
991	2	6.5	38	1	EXE1_HEL SU	P04203	heloderma s
992	2	6.5	38	1	FER_METPR	P81542	metallospa
993	2	6.5	38	1	GLUM_HYDCO	P23063	hydrolagus
994	2	6.5	38	1	GME1_RAT	Q9quz8	rattus norv
995	2	6.5	38	1	H5_COLLI	P02260	columba liv
996	2	6.5	38	1	HIS1_MACFA	P34084	macaca fasc
997	2	6.5	38	1	HMG2_BOVIN	P40673	bos taurus
998	2	6.5	38	1	HOXH_RHOOP	P22661	rhodococcus
999	2	6.5	38	1	ID5B_ADEFA	P09942	adenanthera
1000	2	6.5	38	1	ID5B_PROJU	P32734	prosopsis j

ALIGNMENTS

RESULT 1

FABI_RHASA

ID FABI_RHASA STANDARD; PRT; 33 AA.
AC P81175;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Fatty acid-binding protein, intestinal (I-FABP) (FABPI) (Fragments).
OS Rhamdia sapo.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
OC Pimelodidae; Rhamdia.
OX NCBI_TaxID=55673;
RN [1]
RP SEQUENCE.
RC TISSUE=Intestine;
RX MEDLINE=98036128; PubMed=9370361;
RA Di Pietro S.M., Dell'Angelica E.C., Veerkamp J.H., Sterin-Speziale N.,
RA Santome J.A.;
RT "Amino acid sequence, binding properties and evolutionary
RT relationships of the basic liver fatty-acid-binding protein from the
RT catfish Rhamdia sapo.";
RL Eur. J. Biochem. 249:510-517(1997).
CC -!- FUNCTION: FABP ARE THOUGHT TO PLAY A ROLE IN THE INTRACELLULAR
CC TRANSPORT OF LONG-CHAIN FATTY ACIDS AND THEIR ACYL-COA ESTERS.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC -!- TISSUE SPECIFICITY: INTESTINE.
CC -!- SIMILARITY: BELONGS TO THE FABP/P2/CRBP/CRABP FAMILY OF
CC TRANSPORTERS.
DR InterPro; IPR000463; Fatty_acid_BP.
DR PROSITE; PS00214; FABP; PARTIAL.
KW Transport; Lipid-binding.
FT NON_TER 1 1
FT NON_CONS 12 13
FT NON_CONS 20 21
FT NON_CONS 28 29
FT NON_TER 33 33
SQ SEQUENCE 33 AA; 3660 MW; 5BA16CC2880B7819 CRC64;

Query Match 16.1%; Score 5; DB 1; Length 33;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SVSEI 5
 |||||
 Db 13 SVSEI 17

RESULT 2

DMD_RAT

ID DMD_RAT STANDARD; PRT; 29 AA.
 AC P11530;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Dystrophin (Fragment).
 GN DMD.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88122671; PubMed=3340214;
 RA Nudel U., Robzyk K., Yaffe D.;
 RT "Expression of the putative Duchenne muscular dystrophy gene in
 RT differentiated myogenic cell cultures and in the brain.";
 RL Nature 331:635-638(1988).
 CC -!- FUNCTION: May play a role in anchoring the cytoskeleton to the
 CC plasma membrane.
 CC -!- SUBUNIT: Interacts with the syntrophins SNTA1, SNTB1, SNTB2, SNTG1
 CC and SNTG2 (By similarity).
 CC -----
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 CC -----
 DR EMBL; X07000; CAA30057.1; -.
 DR PIR; S01614; S01614.
 DR InterPro; IPR001589; Actbind_actnin.
 DR InterPro; IPR001202; WW_Rsp5_WWP.
 DR PROSITE; PS00019; ACTININ_1; PARTIAL.
 DR PROSITE; PS00020; ACTININ_2; PARTIAL.
 DR PROSITE; PS01159; WW_DOMAIN_1; PARTIAL.
 DR PROSITE; PS50020; WW_DOMAIN_2; PARTIAL.
 KW Structural protein; Actin-binding; Calcium-binding; Cytoskeleton;
 KW Repeat.
 FT NON_TER 1 1
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3289 MW; 8ECFB28A1A7ACAF0 CRC64;

Query Match 12.9%; Score 4; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQD 30
|||
Db 12 KLQD 15

RESULT 3

PSBY_SYNY3

ID PSBY_SYNY3 STANDARD; PRT; 39 AA.
AC P73676;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Photosystem II protein Y.
GN PSBY OR SML0007.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synechocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugiura M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K., Okumura S.,
RA Shimpo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions."
RL DNA Res. 3:109-136(1996).
CC -!- FUNCTION: MANGANESE-BINDING POLYPEPTIDE WITH L-ARGININE
CC METABOLIZING ENZYME ACTIVITY. COMPONENT OF THE CORE OF PHOTOSYSTEM
CC II (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CELLULAR THYLAKOID MEMBRANE.
CC -!- SIMILARITY: BELONGS TO THE PSBY FAMILY.
CC -----
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CC -----
DR EMBL; D90908; BAA17722.1; -.
DR PIR; S77164; S77164.
KW Photosystem II; Transmembrane; Thylakoid; Complete proteome.
FT TRANSMEM 5 25 POTENTIAL.
SQ SEQUENCE 39 AA; 4202 MW; 3EA176ABAA79F6DF CRC64;

Query Match 12.9%; Score 4; DB 1; Length 39;
Best Local Similarity 100.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQDV 31
 ||||
 Db 31 LQDV 34

RESULT 4

SR1C_SARPE

ID SR1C_SARPE STANDARD; PRT; 39 AA.
 AC P08377;
 DT 01-AUG-1988 (Rel. 08, Created)
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sarcotoxin IC.
 OS Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Sarcophagidae; Sarcophaga.
 OX NCBI_TaxID=7386;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=85207747; PubMed=3888997;
 RA Okada M., Natori S.;
 RT "Primary structure of sarcotoxin I, an antibacterial protein induced
 RT in the hemolymph of Sarcophaga peregrina (flesh fly) larvae.";
 RL J. Biol. Chem. 260:7174-7177(1985).
 CC -!- FUNCTION: SARCOTOXINS, WHICH ARE POTENT BACTERICIDAL PROTEINS,
 CC ARE PRODUCED IN RESPONSE TO INJURY. THEY ARE CYTOTOXIC TO BOTH
 CC GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.
 DR PIR; C22625; CKFHCS.
 DR InterPro; IPR000875; Cecropin.
 DR InterPro; IPR003253; Sarctxn_cecrpn.
 DR Pfam; PF00272; cecropin; 1.
 DR ProDom; PD001670; Sarctxn_cecrpn; 1.
 DR PROSITE; PS00268; CECROPIN; 1.
 KW Insect immunity; Antibiotic; Hemolymph; Amidation; Multigene family.
 FT MOD_RES 39 39 AMIDATION.
 SQ SEQUENCE 39 AA; 4227 MW; 11E79F4F405E855A CRC64;

Query Match 12.9%; Score 4; DB 1; Length 39;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 WLRK 26
 ||||
 Db 2 WLRK 5

RESULT 5

CH60_MYCSM

ID CH60_MYCSM STANDARD; PRT; 28 AA.
 AC P80673;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60 kDa chaperonin (Protein Cpn60) (groEL protein) (Fragment).

GN GROL OR GROEL OR MOPA.
 OS Mycobacterium smegmatis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.
 OX NCBI_TaxID=1772;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=ATCC 607 / mc(2)6 / NRRL B-692;
 RX MEDLINE=97387814; PubMed=9243799;
 RA Lundrigan M.D., Arceneaux J.E.L., Zhu W., Byers B.R.;
 RT "Enhanced hydrogen peroxide sensitivity and altered stress protein
 RT expression in iron-starved Mycobacterium smegmatis.";
 RL BioMetals 10:215-225(1997).
 CC -!- FUNCTION: Prevents misfolding and promotes the refolding and
 CC proper assembly of unfolded polypeptides generated under stress
 CC conditions.
 CC -!- SUBUNIT: Oligomer of 14 subunits composed of two stacked rings of
 CC 7 subunits (By similarity).
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: Belongs to the chaperonin (HSP60) family.
 DR HAMAP; MF_00600; -; 1.
 DR InterPro; IPR001844; Chprnin_Cpn60.
 DR PROSITE; PS00296; CHAPERONINS_CPN60; PARTIAL.
 KW Chaperone; ATP-binding.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3047 MW; 2F40F27B94EF8720 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 18 LNS 20

RESULT 6

COXB_SOLTU

ID COXB_SOLTU STANDARD; PRT; 28 AA.
 AC P80499;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Cytochrome c oxidase polypeptide Vb (EC 1.9.3.1) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Tuber;
 RX MEDLINE=97077345; PubMed=8919912;
 RA Jansch L., Krufft V., Schmitz U.K., Braun H.P.;
 RT "New insights into the composition, molecular mass and stoichiometry
 RT of the protein complexes of plant mitochondria.";
 RL Plant J. 9:357-368(1996).

CC -!- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome
 CC c + 2 H(2)O.
 CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 CC -!- SIMILARITY: BELONGS TO THE CYTOCHROME C OXIDASE VB FAMILY.
 DR InterPro; IPR002124; COX5B.
 DR PROSITE; PS00848; COX5B; PARTIAL.
 KW Oxidoreductase; Inner membrane; Mitochondrion.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 3101 MW; 1EAFA79E2682849C CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VSE 4
 |||
 Db 2 VSE 4

RESULT 7

GUN_SCHCO
 ID GUN_SCHCO STANDARD; PRT; 28 AA.
 AC P81190;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
 DE (Fragment).
 OS Schizophyllum commune (Bracket fungus).
 OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
 OC Agaricales; Schizophyllaceae; Schizophyllum.
 OX NCBI_TaxID=5334;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=97459758; PubMed=9315718;
 RA Clarke A.J., Drummelsmith J., Yaguchi M.;
 RT "Identification of the catalytic nucleophile in the cellulase from
 RT Schizophyllum commune and assignment of the enzyme to Family 5,
 RT subtype 5 of the glycosidases."
 RL FEBS Lett. 414:359-361(1997).
 CC -!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 CC linkages in cellulose, lichenin and cereal beta-D-glucans.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a lipid anchor
 CC (Probable).
 CC -!- SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
 CC HYDROLASES).
 DR InterPro; IPR001547; Glyco_hydro_5.
 DR PROSITE; PS00659; GLYCOSYL_HYDROL_F5; PARTIAL.
 KW Cellulose degradation; Hydrolase; Glycosidase; Zymogen; Membrane;
 KW Lipoprotein.
 FT ACT_SITE 20 20 NUCLEOPHILE.
 FT NON_TER 28 28
 SQ SEQUENCE 28 AA; 2937 MW; B3F1C0C99C9950BE CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 7 EWL 9

RESULT 8

PA23_TRIST

ID PA23_TRIST STANDARD; PRT; 28 AA.
AC P82894;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2, basic 3 (EC 3.1.1.4) (PA2-III) (PLA2-III)
DE (Phosphatidylcholine 2-acylhydrolase) (Fragment).
OS Trimeresurus stejnegeri (Chinese green tree viper).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Viperidae; Crotalinae; Trimeresurus.
OX NCBI_TaxID=39682;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RA Li S.Y., Wang W.Y., Xiong Y.L.;
RT "Isolation, sequence and characterization of five variants of
RT phospholipase A2 from venom of snake Trimeresurus stejnegeri.";
RL Submitted (DEC-2000) to the SWISS-PROT data bank.
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides. Hemolytic and neurotoxic
CC activities are not detected.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP II
CC SUBFAMILY.
DR HSSP; P82287; 1QLL.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3023 MW; 042104521CA1F103 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
|||
Db 5 LGK 7

RESULT 9

PA2C_PSEPO

ID PA2C_PSEPO STANDARD; PRT; 28 AA.
AC P20260;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phospholipase A2 (EC 3.1.1.4) (Pseudexin C chain) (Phosphatidylcholine
DE 2-acylhydrolase) (Fragment).
OS Pseudechis porphyriacus (Red-bellied black snake).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Acanthophiinae; Pseudechis.
OX NCBI_TaxID=8671;
RN [1]
RP SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=89388835; PubMed=2675391;
RA Schmidt J.J., Middlebrook J.L.;
RT "Purification, sequencing and characterization of pseudexin
RT phospholipases A2 from Pseudechis porphyriacus (Australian
RT red-bellied black snake).";
RL Toxicon 27:805-818(1989).
CC -!- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
CC acyl groups in 3-sn-phosphoglycerides.
CC -!- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
CC acylglycerophosphocholine + a fatty acid anion.
CC -!- COFACTOR: Binds 1 calcium ion per subunit (By similarity).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE PHOSPHOLIPASE A2 FAMILY. GROUP I
CC SUBFAMILY.
DR PIR; C32416; C32416.
DR HSSP; P00592; 2PHI.
DR InterPro; IPR001211; PhospholipaseA2.
DR Pfam; PF00068; phoslip; 1.
DR ProDom; PD000303; PhospholipaseA2; 1.
DR PROSITE; PS00119; PA2_ASP; PARTIAL.
DR PROSITE; PS00118; PA2_HIS; PARTIAL.
KW Hydrolase; Lipid degradation; Calcium; Multigene family.
FT NON_TER 28 28
SQ SEQUENCE 28 AA; 3210 MW; 5089A7E85CAA0D5 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 IQL 7
|||
Db 3 IQL 5

RESULT 10

VI03_VACCP
ID VI03_VACCP STANDARD; PRT; 28 AA.
AC Q00334;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE Protein I3 (Fragment).

GN I3L.
 OS Vaccinia virus (strain L-IVP).
 OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
 OC Orthopoxvirus.
 OX NCBI_TaxID=31531;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91066899; PubMed=2250685;
 RA Ryazankina O.I., Shchelkunov S.N., Muravlev A.I., Netesova N.A.,
 RA Mikryukov N.N., Gutorov V.V., Nikulin A.E., Kulichkov V.A.,
 RA Malygin E.G.;
 RT "Molecular-biological study of vaccinia virus genome. II.
 RT Localization and nucleotide sequence of vaccinia virus genes coding
 RT for proteins 36K and 12K.";
 RL Mol. Biol. (Mosk) 24:968-976(1990).
 CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS
 CC THE LATE PHASE OF INFECTION.
 CC -----
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 CC -----
 DR EMBL; X61165; CAA43473.1; -.
 DR InterPro; IPR006754; Pox_I3.
 DR Pfam; PF04661; Pox_I3; 1.
 KW Early protein; Late protein.
 FT NON_TER 1 1
 SQ SEQUENCE 28 AA; 3238 MW; CE10813AC544F010 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 10 NLG 12
 |||
 Db 5 NLG 7

RESULT 11

VIP_ALLMI

ID VIP_ALLMI STANDARD; PRT; 28 AA.
 AC P48142; P01285;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 GN VIP.
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.

RC TISSUE=Stomach;
 RX MEDLINE=93324451; PubMed=8101369;
 RA Wang Y., Conlon J.M.;
 RT "Neuroendocrine peptides (NPY, GRP, VIP, somatostatin) from the brain
 RT and stomach of the alligator.";
 RL Peptides 14:573-579(1993).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 12

VIP_RANRI
 ID VIP_RANRI STANDARD; PRT; 28 AA.
 AC P81016;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Vasoactive intestinal peptide (VIP).
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
 CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
 CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH
 CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR PROSITE; PS00260; GLUCAGON; 1.

KW Glucagon family; Amidation; Hormone.
FT MOD_RES 28 28 AMIDATION.
SQ SEQUENCE 28 AA; 3320 MW; 17B42D7573FF6F37 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
Best Local Similarity 100.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 23 LNS 25

RESULT 13

VIP_SHEEP

ID VIP_SHEEP STANDARD; PRT; 28 AA.
AC P04565;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Vasoactive intestinal peptide (VIP).
GN VIP.
OS Ovis aries (Sheep),
OS Capra hircus (Goat), and
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940, 9925, 9615;
RN [1]
RP SEQUENCE.
RC SPECIES=Sheep; TISSUE=Brain;
RX MEDLINE=91045331; PubMed=2235680;
RA Gafvelin G.;
RT "Isolation and primary structure of VIP from sheep brain.";
RL Peptides 11:703-706(1990).
RN [2]
RP SEQUENCE.
RC SPECIES=Sheep; TISSUE=Small intestine;
RX MEDLINE=91239834; PubMed=2034821;
RA Bounjoua Y., Vandermeers A., Robberecht P., Vandermeers-Piret M.C.,
RA Christophe J.;
RT "Purification and amino acid sequence of vasoactive intestinal
RT peptide, peptide histidine isoleucinamide and secretin from the ovine
RT small intestine.";
RL Regul. Pept. 32:169-179(1991).
RN [3]
RP SEQUENCE.
RC SPECIES=C.hircus, and C.familiaris;
RX MEDLINE=86313167; PubMed=3748846;
RA Eng J., Du B.-H., Raufman J.-P., Yalow R.S.;
RT "Purification and amino acid sequences of dog, goat and guinea pig
RT VIPs.";
RL Peptides 7 Suppl. 1:17-20(1986).
CC -!- FUNCTION: VIP CAUSES VASODILATION, LOWERS ARTERIAL BLOOD
CC PRESSURE, STIMULATES MYOCARDIAL CONTRACTILITY, INCREASES
CC GLYCOGENOLYSIS AND RELAXES THE SMOOTH MUSCLE OF TRACHEA, STOMACH

CC AND GALL BLADDER.
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; A60304; A60304.
 DR PIR; B60072; VRSH.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR PRINTS; PR00275; GLUCAGON.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation; Hormone.
 FT MOD_RES 28 28 AMIDATION.
 SQ SEQUENCE 28 AA; 3327 MW; EF313FB573FF6F3F CRC64;

Query Match 9.7%; Score 3; DB 1; Length 28;
 Best Local Similarity 100.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 23 LNS 25

RESULT 14

GALA_ALLMI

ID GALA_ALLMI STANDARD; PRT; 29 AA.
 AC P47215;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95023390; PubMed=7524049;
 RA Wang Y., Conlon J.M.;
 RT "Purification and primary structure of galanin from the alligator
 RT stomach.";
 RL Peptides 15:603-606(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3216 MW; E02F019B2D3E0529 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 15

GALA_AMICA

ID GALA_AMICA STANDARD; PRT; 29 AA.
AC P47214;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
OS Amia calva (Bowfin).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Amiiformes; Amiidae; Amia.
OX NCBI_TaxID=7924;
RN [1]
RP SEQUENCE.
RC TISSUE=Stomach;
RX MEDLINE=95083480; PubMed=7527531;
RA Wang Y., Conlon J.M.;
RT "Purification and characterization of galanin from the
RT phylogenetically ancient fish, the bowfin (*Amia calva*) and dogfish
RT (*Scyliorhinus canicula*).";
RL Peptides 15:981-986(1994).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3114 MW; 7518719B2D271627 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
|||
Db 4 LNS 6

RESULT 16

GALA_CHICK

ID GALA_CHICK STANDARD; PRT; 29 AA.
AC P30802;
DT 01-JUL-1993 (Rel. 26, Created)

DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 GN GAL OR GALN.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=91348254; PubMed=1715289;
 RA Norberg A., Sillard R., Carlquist M., Joernvall H., Mutt V.;
 RT "Chemical detection of natural peptides by specific structures.
 RT Isolation of chicken galanin by monitoring for its N-terminal
 RT dipeptide, and determination of the amino acid sequence.";
 RL FEBS Lett. 288:151-153(1991).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR PIR; S17147; S17147.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR PRINTS; PR00273; GALANIN.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3212 MW; EB66919B2D271629 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 17

GALA_ONCMY

ID GALA_ONCMY STANDARD; PRT; 29 AA.
 AC P47213;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]

RP SEQUENCE.
 RC TISSUE=Stomach;
 RX MEDLINE=95164756; PubMed=7532194;
 RA Anglade I., Wang Y., Jensen J., Tramu G., Kah O., Conlon J.M.;
 RT "Characterization of trout galanin and its distribution in trout
 RT brain and pituitary.";
 RL J. Comp. Neurol. 350:63-74(1994).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.
 DR ProDom; PD005962; Galanin; 1.
 DR PROSITE; PS00861; GALANIN; 1.
 KW Hormone; Neuropeptide; Amidation.
 FT MOD_RES 29 29 AMIDATION.
 SQ SEQUENCE 29 AA; 3044 MW; 73C37190403FA349 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
 |||
 Db 4 LNS 6

RESULT 18
 GALA_RANRI
 ID GALA_RANRI STANDARD; PRT; 29 AA.
 AC P47216;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Galanin.
 OS Rana ridibunda (Laughing frog) (Marsh frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidea; Ranidae; Rana.
 OX NCBI_TaxID=8406;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=95309202; PubMed=7540547;
 RA Chartrel N., Wang Y., Fournier A., Vaudry H., Conlon J.M.;
 RT "Frog vasoactive intestinal polypeptide and galanin: primary
 RT structures and effects on pituitary adenylate cyclase.";
 RL Endocrinology 136:3079-3086(1995).
 CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
 CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
 CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
 CC SECRETION.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
 DR InterPro; IPR001600; Galanin.
 DR Pfam; PF01296; Galanin; 1.

DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3162 MW; F718719B2D3FB529 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
|||
Db 4 LNS 6

RESULT 19

GALA_SHEEP

ID GALA_SHEEP STANDARD; PRT; 29 AA.
AC P31234;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galanin.
GN GAL OR GALN OR GLNN.
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID=9940;
RN [1]
RP SEQUENCE.
RC TISSUE=Brain;
RX MEDLINE=92158824; PubMed=1724081;
RA Sillard R., Langel U., Joernvall H.;
RT "Isolation and characterization of galanin from sheep brain.";
RL Peptides 12:855-859(1991).
CC -!- FUNCTION: CONTRACTS SMOOTH MUSCLE OF THE GASTROINTESTINAL AND
CC GENITOURINARY TRACT, REGULATES GROWTH HORMONE RELEASE, MODULATES
CC INSULIN RELEASE, AND MAY BE INVOLVED IN THE CONTROL OF ADRENAL
CC SECRETION.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE GALANIN FAMILY.
DR InterPro; IPR001600; Galanin.
DR Pfam; PF01296; Galanin; 1.
DR PRINTS; PR00273; GALANIN.
DR ProDom; PD005962; Galanin; 1.
DR PROSITE; PS00861; GALANIN; 1.
KW Hormone; Neuropeptide; Amidation.
FT MOD_RES 29 29 AMIDATION.
SQ SEQUENCE 29 AA; 3185 MW; F718719B2D3FB089 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 LNS 17
|||

Db

4 LNS 6

RESULT 20

GLUC_CHIBR

ID GLUC_CHIBR STANDARD; PRT; 29 AA.
AC P31297;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucagon.
GN GCG.
OS Chinchilla brevicaudata (Chinchilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Chinchillidae;
OC Chinchilla.
OX NCBI_TaxID=10152;
RN [1]
RP SEQUENCE.
RX MEDLINE=91045327; PubMed=2235678;
RA Eng J., Kleinman W.A., Chu L.S.;
RT "Purification of peptide hormones from chinchilla pancreas by
RT chemical assay."
RL Peptides 11:683-685(1990).
CC -!- FUNCTION: PROMOTES HYDROLYSIS OF GLYCOGEN AND LIPIDS, AND RAISES
CC THE BLOOD SUGAR LEVEL.
CC -!- INDUCTION: PRODUCED IN THE A CELLS OF THE ISLETS OF LANGERHANS
CC IN RESPONSE TO A DROP IN BLOOD SUGAR CONCENTRATION.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR; A60413; GCCB.
DR HSSP; P01275; 1BH0.
DR InterPro; IPR000532; Glucagon.
DR Pfam; PF00123; hormone2; 1.
DR PRINTS; PR00275; GLUCAGON.
DR SMART; SM00070; GLUCA; 1.
DR PROSITE; PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone.
SQ SEQUENCE 29 AA; 3478 MW; 19ECF4DABB752B27 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 5.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KHL 15

|||

Db 12 KHL 14

RESULT 21

IPYR_DESVH

ID IPYR_DESVH STANDARD; PRT; 29 AA.
AC P19371;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Inorganic pyrophosphatase (EC 3.6.1.1) (Pyrophosphate phospho-
DE hydrolase) (PPase) (Fragment).

OS Desulfovibrio vulgaris (strain Hildenborough).
 OC Bacteria; Proteobacteria; Deltaproteobacteria; Desulfovibrionales;
 OC Desulfovibrionaceae; Desulfovibrio.
 OX NCBI_TaxID=882;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90365722; PubMed=2168174;
 RA Liu M.-Y., le Gall J.;
 RT "Purification and characterization of two proteins with inorganic
 RT pyrophosphatase activity from Desulfovibrio vulgaris: rubrerythrin
 RT and a new, highly active, enzyme."
 RL Biochem. Biophys. Res. Commun. 171:313-318(1990).
 CC -!- FUNCTION: INORGANIC PYROPHOSPHATASE IS AN ESSENTIAL ENZYME FOR THE
 CC ACTIVATION OF SULFATE BY SULFATE REDUCING BACTERIA. THIS IS A HIGH
 CC ACTIVITY PYROPHOSPHATASE.
 CC -!- CATALYTIC ACTIVITY: Diphosphate + H(2)O = 2 phosphate.
 CC -!- SUBCELLULAR LOCATION: Periplasmic (Potential).
 DR PIR; A35687; A35687.
 DR HAMAP; MF_00209; -; 1.
 DR InterPro; IPR001596; Pyrophosphatase.
 DR PROSITE; PS00387; PPASE; PARTIAL.
 KW Hydrolase; Periplasmic.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3201 MW; 3FC5792360F2227B CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 SEI 5
 |||
 Db 15 SEI 17

RESULT 22

NUO1_SOLTU

ID NUO1_SOLTU STANDARD; PRT; 29 AA.
 AC P80267;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE NADH-ubiquinone oxidoreductase 14 kDa subunit (EC 1.6.5.3)
 DE (EC 1.6.99.3) (Complex I-14KD) (CI-14KD) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; lamiids; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=cv. Bintje; TISSUE=Tuber;
 RX MEDLINE=94124587; PubMed=8294484;
 RA Herz U., Schroeder W., Liddell A., Leaver C.J., Brennicke A.,
 RA Grohmann L.;
 RT "Purification of the NADH:ubiquinone oxidoreductase (complex I) of
 RT the respiratory chain from the inner mitochondrial membrane of
 RT Solanum tuberosum.";

RL J. Biol. Chem. 269:2263-2269(1994).
 CC -!- FUNCTION: TRANSFER OF ELECTRONS FROM NADH TO THE RESPIRATORY
 CC CHAIN. THE IMMEDIATE ELECTRON ACCEPTOR FOR THE ENZYME IS BELIEVED
 CC TO BE UBIQUINONE.
 CC -!- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
 CC -!- CATALYTIC ACTIVITY: NADH + acceptor = NAD(+) + reduced acceptor.
 CC -!- SUBUNIT: COMPLEX I IS COMPOSED OF ABOUT 30 DIFFERENT SUBUNITS.
 CC -!- SUBCELLULAR LOCATION: MATRIX SIDE OF THE MITOCHONDRIAL INNER
 CC MEMBRANE.
 DR PIR; I49732; I49732.
 KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3269 MW; E2B4DFB558D423D4 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 25 RKK 27
 |||
 Db 2 RKK 4

RESULT 23

P2SM_LOXIN
 ID P2SM_LOXIN STANDARD; PRT; 29 AA.
 AC P83046;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Sphingomyelinase P2 (EC 3.1.4.12) (Fragment).
 OS Loxosceles intermedia (Spider).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
 OC Araneomorphae; Haplogynae; Sicariidae; Loxosceles.
 OX NCBI_TaxID=58218;
 RN [1]
 RP SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, COFACTOR, SUBCELLULAR
 RP LOCATION, AND TISSUE SPECIFICITY.
 RC TISSUE=Venom;
 RX MEDLINE=99009277; PubMed=9790962;
 RA Tambourgi D.V., Magnoli F.C., van den Berg C.W., Morgan B.P.,
 RA de Araujo P.S., Alves E.W., Da Silva W.D.;
 RT "Sphingomyelinases in the venom of the spider Loxosceles intermedia
 RT are responsible for both dermonecrosis and complement-dependent
 RT hemolysis.";
 RL Biochem. Biophys. Res. Commun. 251:366-373(1998).
 CC -!- FUNCTION: Has sphingomyelinase activity. Induces complement-
 CC dependent hemolysis and dermonecrosis.
 CC -!- CATALYTIC ACTIVITY: Sphingomyelin + H(2)O = N-acylsphingosine +
 CC choline phosphate.
 CC -!- COFACTOR: Calcium ion.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
 KW Hydrolase; Toxin; Calcium; Hemolysis.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 3281 MW; 4488EDD619BD2398 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 NLG 12
|||
Db 25 NLG 27

RESULT 24

PCG4_PACGO

ID PCG4_PACGO STANDARD; PRT; 29 AA.
AC P82417;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G4.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii."
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: HAS ACTIVITY AGAINST SOME GRAM-POSITIVE BACTERIA
CC AND S.CEREVISIAE. HAS A NON-HEMOLYTIC ACTIVITY.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3163.87; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 29 AA; 3165 MW; 7037D0B855072AF8 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 EWL 24
|||
Db 11 EWL 13

RESULT 25

RS7_METTE

ID RS7_METTE STANDARD; PRT; 29 AA.
AC O93639;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S7P (Fragment).
GN RPS7P OR S7.
OS Methanosarcina thermophila.

OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
 OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
 OX NCBI_TaxID=2210;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DSM 1825 / TM-1;
 RX MEDLINE=99059471; PubMed=9845338;
 RA Thomas T., Cavicchioli R.;
 RT "Archaeal cold-adapted proteins: structural and evolutionary analysis
 RT of the elongation factor 2 proteins from psychrophilic, mesophilic and
 RT thermophilic methanogens.";
 RL FEBS Lett. 439:281-287(1998).
 CC -!- FUNCTION: One of the primary rRNA binding proteins, it binds
 CC directly to 16S rRNA where it nucleates assembly of the head
 CC domain of the 30S subunit. Is located at the subunit interface
 CC close to the decoding center (By similarity).
 CC -!- SUBUNIT: Part of the 30S ribosomal subunit.
 CC -!- SIMILARITY: BELONGS TO THE S7P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 DR EMBL; AF026165; AAC79199.1; -.
 DR PIR; T44245; T44245.
 DR HAMAP; MF_00480; -; 1.
 DR InterPro; IPR000235; Ribosomal_S7.
 DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
 KW Ribosomal protein; RNA-binding; rRNA-binding.
 FT NON_TER 1 1
 SQ SEQUENCE 29 AA; 3217 MW; 1602B8A2E6C50C2B CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 22 ERV 24

RESULT 26

SODC_OLEEU

ID SODC_OLEEU STANDARD; PRT; 29 AA.
 AC P80740;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Superoxide dismutase [Cu-Zn] (EC 1.15.1.1) (Allergen Ole e 5) (Ole e
 DE V) (Fragment).
 OS Olea europaea (Common olive).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

OC Asteridae; lamiids; Lamiales; Oleaceae; Olea.
 OX NCBI_TaxID=4146;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=98160390; PubMed=9500754;
 RA Boluda L., Alonso C., Fernandez-Caldas E.;
 RT "Purification, characterization, and partial sequencing of two new
 RT allergens of Olea europaea.";
 RL J. Allergy Clin. Immunol. 101:210-216(1998).
 CC -!- FUNCTION: Destroys radicals which are normally produced within the
 CC cells and which are toxic to biological systems (By similarity).
 CC -!- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
 CC -!- COFACTOR: Binds 1 copper ion and 1 zinc ion per subunit (By
 CC similarity).
 CC -!- SIMILARITY: BELONGS TO THE CU-ZN SUPEROXIDE DISMUTASE FAMILY.
 DR InterPro; IPR001424; SOD_CU_ZN.
 DR Pfam; PF00080; sodcu; 1.
 DR PROSITE; PS00087; SOD_CU_ZN_1; PARTIAL.
 DR PROSITE; PS00332; SOD_CU_ZN_2; PARTIAL.
 KW Antioxidant; Oxidoreductase; Metal-binding; Copper; Zinc; Allergen.
 FT NON_TER 29 29
 SQ SEQUENCE 29 AA; 2973 MW; 836C7A193EDAD71E CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 15 LNS 17
 |||
 Db 7 LNS 9

RESULT 27

TL16_SPIOL

ID TL16_SPIOL STANDARD; PRT; 29 AA.
 AC P81834;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Thylakoid lumenal 16.5 kDa protein (P16.5) (Fragment).
 OS Spinacia oleracea (Spinach).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
 OX NCBI_TaxID=3562;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Leaf;
 RX MEDLINE=98175931; PubMed=9506969;
 RA Kieselbach T., Hagman A., Andersson B., Schroeder W.P.;
 RT "The thylakoid lumen of chloroplasts. Isolation and
 RT characterization.";
 RL J. Biol. Chem. 273:6710-6716(1998).
 CC -!- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
 KW Chloroplast; Thylakoid.
 FT NON_TER 29 29

SQ SEQUENCE 29 AA; 3464 MW; 58B785764E2623E3 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 29;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 25 RKK 27
|||
Db 19 RKK 21

RESULT 28

DMS3_PHYSA

ID DMS3_PHYSA STANDARD; PRT; 30 AA.
AC P80279;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Dermaseptin 3 (DS III).
OS Phyllomedusa sauvagei (Sauvage's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Hylidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8395;
RN [1]
RP SEQUENCE.
RC TISSUE=Skin secretion;
RX MEDLINE=94139686; PubMed=8306981;
RA Mor A., Nicolas P.;
RT "Isolation and structure of novel defensive peptides from frog skin."
RL Eur. J. Biochem. 219:145-154(1994).
CC -!- FUNCTION: POSSESSES A POTENT ANTIMICROBIAL ACTIVITY AGAINST
CC BACTERIA FUNGI AND PROTOZOA. PROBABLY ACTS BY DISTURBING MEMBRANE
CC FUNCTIONS WITH ITS AMPHIPATIC STRUCTURE.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Skin.
CC -!- SIMILARITY: Belongs to the frog skin active peptide (FSAP) family.
CC Dermaseptin subfamily.
KW Amphibian defense peptide; Antibiotic; Fungicide; Multigene family.
SQ SEQUENCE 30 AA; 3024 MW; FD5F190C3DCBB0D7 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 23 KKL 25

RESULT 29

FTN_BACFR

ID FTN_BACFR STANDARD; PRT; 30 AA.
AC P28733;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ferritin like protein (Fragment).
 OS Bacteroides fragilis.
 OC Bacteria; Bacteroidetes; Bacteroides (class); Bacteroidales;
 OC Bacteroidaceae; Bacteroides.
 OX NCBI_TaxID=817;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=20656-2-1;
 RX MEDLINE=92406001; PubMed=1526453;
 RA Rocha E.R., Andrews S.C., Keen J.N., Brock J.H.;
 RT "Isolation of a ferritin from Bacteroides fragilis.";
 RL FEMS Microbiol. Lett. 74:207-212(1992).
 CC -!- FUNCTION: MAY ALLEVIATE IRON TOXICITY IN THE PRESENCE OF
 CC OXYGEN.
 CC -!- COFACTOR: BINDS ABOUT THREE IRON ATOMS PER MOLECULE.
 CC -!- SUBUNIT: FORMS OLIGOMERS OF ABOUT 400 kDa (THE MONOMER IS ABOUT
 CC 17 kDa).
 CC -!- SIMILARITY: BELONGS TO THE FERRITIN FAMILY. PROKARYOTIC SUBFAMILY.
 CC -!- SIMILARITY: Contains 1 ferritin-like diiron domain.
 DR InterPro; IPR001519; Ferritin.
 DR Pfam; PF00210; ferritin; 1.
 DR PROSITE; PS50905; FERRITIN LIKE; 1.
 KW Iron storage; Iron; Metal-binding.
 FT DOMAIN 1 >30 FERRITIN-LIKE DIIRON.
 FT METAL 17 17 IRON (BY SIMILARITY).
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3529 MW; C70505B5696EFC4F CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 27 KLQ 29
 |||
 Db 5 KLQ 7

RESULT 30

GLUM_ANGAN

ID GLUM_ANGAN STANDARD; PRT; 30 AA.
 AC P41521;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glucagon-like peptide (GLP).
 OS Anguilla anguilla (European freshwater eel), and
 OS Anguilla rostrata (American eel).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Anguilliformes; Anguillidae;
 OC Anguilla.
 OX NCBI_TaxID=7936, 7938;
 RN [1]
 RP SEQUENCE.
 RC SPECIES=A.anguilla, and A.rostrata;
 RC TISSUE=Pancreas;
 RX MEDLINE=91340068; PubMed=1874385;
 RA Conlon J.M., Andrews P.C., Thim L., Moon T.W.;

RT "The primary structure of glucagon-like peptide but not insulin has
 RT been conserved between the American eel, *Anguilla rostrata* and the
 RT European eel, *Anguilla anguilla*.";
 RL Gen. Comp. Endocrinol. 82:23-32(1991).
 CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR; B61125; B61125.
 DR PIR; C61125; C61125.
 DR HSSP; P01275; 1BH0.
 DR InterPro; IPR000532; Glucagon.
 DR Pfam; PF00123; hormone2; 1.
 DR SMART; SM00070; GLUCA; 1.
 DR PROSITE; PS00260; GLUCAGON; 1.
 KW Glucagon family; Amidation.
 FT MOD_RES 30 30 AMIDATION.
 SQ SEQUENCE 30 AA; 3376 MW; 592DA5EABD6E49D0 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 28 LQD 30
 |||
 Db 14 LQD 16

RESULT 31

OTCC_AERPU

ID OTCC_AERPU STANDARD; PRT; 30 AA.
 AC P11726;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Ornithine carbamoyltransferase, catabolic (EC 2.1.3.3) (OTCase)
 DE (Fragment).
 OS *Aeromonas punctata* (*Aeromonas caviae*).
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
 OC Aeromonadaceae; *Aeromonas*.
 OX NCBI_TaxID=648;
 RN [1]
 RP SEQUENCE.
 RC STRAIN=NCIB 9232;
 RX MEDLINE=85104799; PubMed=3968036;
 RA Falmagne P., Portetelle D., Stalon V.;
 RT "Immunological and structural relatedness of catabolic ornithine
 RT carbamoyltransferases and the anabolic enzymes of enterobacteria.";
 RL J. Bacteriol. 161:714-719(1985).
 CC -!- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine = phosphate
 CC + L-citrulline.
 CC -!- PATHWAY: Arginine degradation via arginine deiminase; second step.
 CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
 DR InterPro; IPR006130; Asp/Orn_COtranf.
 DR InterPro; IPR006132; OTCace_P.
 DR Pfam; PF02729; OTCace_N; 1.
 DR PROSITE; PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
 KW Transferase; Arginine metabolism.
 FT NON_TER 30 30

SQ SEQUENCE 30 AA; 3654 MW; 673CB989FE72F9C1 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 EIQ 6
|||
Db 19 EIQ 21

RESULT 32

PCG2_PACGO

ID PCG2_PACGO STANDARD; PRT; 30 AA.
AC P82415;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Ponericin G2.
OS Pachycondyla goeldii (Ponerine ant).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
OC Ponerinae; Pachycondyla.
OX NCBI_TaxID=118888;
RN [1]
RP SEQUENCE, AND FUNCTION.
RC TISSUE=Venom;
RX MEDLINE=21264562; PubMed=11279030;
RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
RA Longeon A., Chafotte A., Dejean A., Rossier J.;
RT "Ponericins, new antibacterial and insecticidal peptides from the
RT venom of the ant Pachycondyla goeldii."
RL J. Biol. Chem. 276:17823-17829(2001).
CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
CC AND NON-HEMOLYTIC ACTIVITIES.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- MASS SPECTROMETRY: MW=3306.56; METHOD=MALDI.
KW Antibiotic; Insect immunity; Fungicide.
SQ SEQUENCE 30 AA; 3308 MW; A12CD4D0BAF40B5D CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
|||
Db 11 EWL 13

RESULT 33

PCG3_PACGO

ID PCG3_PACGO STANDARD; PRT; 30 AA.
AC P82416;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Ponericin G3.
 OS Pachycondyla goeldii (Ponerine ant).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Formicidae;
 OC Ponerinae; Pachycondyla.
 OX NCBI_TaxID=118888;
 RN [1]
 RP SEQUENCE, AND FUNCTION.
 RC TISSUE=Venom;
 RX MEDLINE=21264562; PubMed=11279030;
 RA Orivel J., Redeker V., Le Caer J.-P., Krier F., Revol-Junelles A.-M.,
 RA Longeon A., Chafotte A., Dejean A., Rossier J.;
 RT "Ponericins, new antibacterial and insecticidal peptides from the
 RT venom of the ant Pachycondyla goeldii.";
 RL J. Biol. Chem. 276:17823-17829(2001).
 CC -!- FUNCTION: BROAD SPECTRUM OF ACTIVITY AGAINST BOTH GRAM-POSITIVE
 CC AND GRAM-NEGATIVE BACTERIA AND S.CEREVISIAE. HAS INSECTICIDAL
 CC AND NON-HEMOLYTIC ACTIVITIES.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- MASS SPECTROMETRY: MW=3381.36; METHOD=MALDI.
 KW Antibiotic; Insect immunity; Fungicide.
 SQ SEQUENCE 30 AA; 3383 MW; BC0463D0AF140B53 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 22 EWL 24
 |||
 Db 11 EWL 13

RESULT 34
 PSAM_PORPU
 ID PSAM_PORPU STANDARD; PRT; 30 AA.
 AC P51395;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE Photosystem I reaction centre subunit XII (PSI-M).
 GN PSAM.
 OS Porphyra purpurea.
 OG Chloroplast.
 OC Eukaryota; Rhodophyta; Bangiophyceae; Bangiales; Bangiaceae; Porphyra.
 OX NCBI_TaxID=2787;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Avonport;
 RA Reith M.E., Munholland J.;
 RT "Complete nucleotide sequence of the Porphyra purpurea chloroplast
 RT genome.";
 RL Plant Mol. Biol. Rep. 13:333-335(1995).
 CC -!- SIMILARITY: BELONGS TO THE PSAM FAMILY.
 CC -----
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DR EMBL; U38804; AAC08281.1; -.
DR PIR; S73316; S73316.
KW Photosystem I; Photosynthesis; Chloroplast.
SQ SEQUENCE 30 AA; 3338 MW; 8D1930479D8A5527 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 11 LGK 13
|||
Db 24 LGK 26

RESULT 35

TX2_THRPR

ID TX2_THRPR STANDARD; PRT; 30 AA.
AC P83476;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Toxin ProTx-II.
OS Thrixopelma pruriens (Green velvet).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Araneae;
OC Mygalomorphae; Theraphosidae; Thrixopelma.
OX NCBI_TaxID=213387;
RN [1]
RP SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, MASS
RP SPECTROMETRY, AND DISULFIDE BONDS.
RC TISSUE=Venom;
RX MEDLINE=22363233; PubMed=12475222;
RA Middleton R.E., Warren V.A., Kraus R.L., Hwang J.C., Liu C.J., Dai G.,
RA Brochu R.M., Kohler M.G., Gao Y.-D., Garsky V.M., Bogusky M.J.,
RA Mehl J.T., Cohen C.J., Smith M.M.;
RT "Two tarantula peptides inhibit activation of multiple sodium
RT channels.";
RL Biochemistry 41:14734-14747(2002).
CC -!- FUNCTION: Inhibits voltage-gated calcium and sodium channels.
CC Shifts the voltage-dependence of channel activation to more
CC positive potentials.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -!- MASS SPECTROMETRY: MW=3827; METHOD=Electrospray.
CC -!- MASS SPECTROMETRY: MW=3827; METHOD=MALDI.
CC -!- SIMILARITY: BELONGS TO THE SPIDER POTASSIUM CHANNEL INHIBITORY
CC TOXIN FAMILY.
KW Toxin; Neurotoxin; Ionic channel inhibitor; Calcium channel inhibitor;
KW Sodium channel inhibitor.
FT DISULFID 2 16
FT DISULFID 9 21
FT DISULFID 15 25
SQ SEQUENCE 30 AA; 3833 MW; 5B8CF4C6338C1B9B CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 27 KKL 29

RESULT 36

UP61_UPEIN

ID UP61_UPEIN STANDARD; PRT; 30 AA.
AC P82037;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 6.1.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
OC Myobatrachinae; Uperoleia.
OX NCBI_TaxID=104953;
RN [1]
RP SEQUENCE, AND MASS SPECTROMETRY.
RC TISSUE=Skin secretion;
RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
RA Adams G.W., Severini C.;
RT "Novel uperin peptides from the dorsal glands of the australian
RT floodplain toadlet Uperoleia inundata.";
RL Aust. J. Chem. 49:475-484(1996).
CC -!- FUNCTION: UNKNOWN.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
CC -!- MASS SPECTROMETRY: MW=3233.85; METHOD=MALDI.
KW Amphibian defense peptide.
SQ SEQUENCE 30 AA; 3233 MW; 4EE15B9EB110F68E CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 24 KKL 26

RESULT 37

UP62_UPEIN

ID UP62_UPEIN STANDARD; PRT; 30 AA.
AC P82038;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Uperin 6.2.
OS Uperoleia inundata (Floodplain toadlet).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Bufonoidea; Myobatrachidae;
 OC Myobatrachinae; Uperoleia.
 OX NCBI_TaxID=104953;
 RN [1]
 RP SEQUENCE, AND MASS SPECTROMETRY.
 RC TISSUE=Skin secretion;
 RA Bradford A.M., Raftery M.J., Bowie J.H., Tyler M.J., Wallace J.C.,
 RA Adams G.W., Severini C.;
 RT "Novel uperin peptides from the dorsal glands of the australian
 RT floodplain toadlet Uperoleia inundata.";
 RL Aust. J. Chem. 49:475-484(1996).
 CC -!- FUNCTION: UNKNOWN.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.
 CC -!- MASS SPECTROMETRY: MW=3261.85; METHOD=MALDI.
 KW Amphibian defense peptide.
 SQ SEQUENCE 30 AA; 3261 MW; 4EE15B9EB10841DE CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
 |||
 Db 24 KKL 26

RESULT 38

VAA2_EQUAR

ID VAA2_EQUAR STANDARD; PRT; 30 AA.
 AC Q04238;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Vacuolar ATP synthase catalytic subunit A, isoform 2 (EC 3.6.3.14)
 DE (Fragment).
 OS Equisetum arvense (Field horsetail) (Common horsetail).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Equisetophyta; Sphenopsida; Equisetales; Equisetaceae; Equisetum.
 OX NCBI_TaxID=3258;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93138084; PubMed=8422915;
 RA Starke T., Gogarten J.P.;
 RT "A conserved intron in the V-ATPase A subunit genes of plants and
 RT algae.";
 RL FEBS Lett. 315:252-258(1993).
 CC -!- FUNCTION: CATALYTIC SUBUNIT OF THE PERIPHERAL V1 COMPLEX OF
 CC VACUOLAR ATPASE. V-ATPASE VACUOLAR ATPASE IS RESPONSIBLE FOR
 CC ACIDIFYING A VARIETY OF INTRACELLULAR COMPARTMENTS IN EUKARYOTIC
 CC CELLS.
 CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + H(+) (In) = ADP + phosphate +
 CC H(+) (Out).
 CC -!- SUBUNIT: V-ATPASE IS AN HETEROMULTIMERIC ENZYME COMPOSED OF A
 CC PERIPHERAL CATALYTIC V1 COMPLEX (MAIN COMPONENTS: SUBUNITS A, B,
 CC C, D, E, AND F) ATTACHED TO AN INTEGRAL MEMBRANE V0 PROTON PORE
 CC COMPLEX (MAIN COMPONENT: THE PROTEOLIPID PROTEIN).

CC -!- MISCELLANEOUS: TWO SEPARATE GENES ENCODE THE CATALYTIC 70 kDa
 CC V-ATPASE SUBUNIT IN PSILOTUM AND EQUISETUM.
 CC -!- SIMILARITY: Belongs to the ATPase alpha/beta chains family.
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 CC -----
 DR EMBL; X56984; CAA40302.1; -.
 DR PIR; S21815; S21815.
 DR InterPro; IPR000194; ATPase_a/bcentre.
 DR PROSITE; PS00152; ATPASE_ALPHA_BETA; PARTIAL.
 KW ATP synthesis; Hydrogen ion transport; Hydrolase; ATP-binding;
 KW Multigene family.
 FT NON_TER 1 1
 FT NON_TER 30 30
 SQ SEQUENCE 30 AA; 3372 MW; 51CCA4A3DA9E5D84 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 18 MER 20
 |||
 Db 23 MER 25

RESULT 39 /
 Y523_BORBU
 ID Y523_BORBU STANDARD; PRT; 30 AA.
 AC 051473;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Hypothetical protein BB0523.
 GN BB0523.
 OS Borrelia burgdorferi (Lyme disease spirochete).
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
 OX NCBI_TaxID=139;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 35210 / B31;
 RX MEDLINE=98065943; PubMed=9403685;
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,
 RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
 RA Utterback T., Wathley L., McDonald L., Artiach P., Bowman C.,
 RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
 RA Smith H.O., Venter J.C.;
 RT "Genomic sequence of a Lyme disease spirochaete, Borrelia
 RT burgdorferi.";

RL Nature 390:580-586(1997).
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 CC -----
 DR EMBL; AE001154; AAC66894.1; -.
 DR PIR; B70165; B70165.
 DR TIGR; BB0523; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 30 AA; 3431 MW; DE437B15D2A48AA8 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 30;
 Best Local Similarity 100.0%; Pred. No. 5.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 19 ERV 21
 |||
 Db 26 ERV 28

RESULT 40

CEC1_PIG

ID CEC1_PIG STANDARD; PRT; 31 AA.
 AC P14661;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Cecropin P1.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=90083227; PubMed=2512577;
 RA Lee J.-Y., Boman A., Chuanxin S., Andersson M., Joernvall H., Mutt V.,
 RA Boman H.G.;
 RT "Antibacterial peptides from pig intestine: isolation of a mammalian
 RT cecropin.";
 RL Proc. Natl. Acad. Sci. U.S.A. 86:9159-9162(1989).
 RN [2]
 RP STRUCTURE BY NMR.
 RX MEDLINE=93011123; PubMed=1396696;
 RA Sipos D., Andersson M., Ehrenberg A.;
 RT "The structure of the mammalian antibacterial peptide cecropin P1 in
 RT solution, determined by proton-NMR.";
 RL Eur. J. Biochem. 209:163-169(1992).
 CC -!- FUNCTION: CECROPINS HAVE LYTIC AND ANTIBACTERIAL ACTIVITY AGAINST
 CC SEVERAL GRAM-POSITIVE AND GRAM-NEGATIVE BACTERIA. ACTS BY A
 CC NONPORE MECHANISM.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- SIMILARITY: BELONGS TO THE CECROPIN FAMILY.

DR PIR; A36221; A36221.
DR InterPro; IPR000875; Cecropin.
DR Pfam; PF00272; cecropin; 1.
DR PROSITE; PS00268; CECROPIN; 1.
KW Antibiotic.
SQ SEQUENCE 31 AA; 3339 MW; CB2B374A8B153850 CRC64;

Query Match 9.7%; Score 3; DB 1; Length 31;
Best Local Similarity 100.0%; Pred. No. 5.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 26 KKL 28
|||
Db 8 KKL 10

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Job time : 6.11838 secs